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(54) METHODS AND COMPOSITIONS FOR WEED CONTROL

VERFAHREN UND ZUSAMMENSETZUNGEN ZUR UNKRAUTBEKÄMPFUNG

MÉTHODES ET COMPOSITIONS POUR LUTTER CONTRE LES MAUVAISES HERBES

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(73) Proprietor: **Monsanto Technology LLC**
St. Louis, MO 63167 (US)

(72) Inventors:
• **FINNESSY, John J.**
St. Louis, Missouri 63167 (US)
• **NAVARRO, Santiago X.**
St. Louis, Missouri 63167 (US)
• **SAMMONS, Robert Douglas**
St. Louis, Missouri 63167 (US)
• **TAO, Nengbing**
St. Louis, Missouri 63167 (US)

(74) Representative: **Uexküll & Stolberg**
Partnerschaft von
Patent- und Rechtsanwälten mbB
Beselerstraße 4
22607 Hamburg (DE)

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Remarks:

The complete document including Reference Tables and the Sequence Listing can be downloaded from the EPO website

Description**FIELD OF THE INVENTION**

[0001] The embodiments described herein relate generally to the field of weed management. More specifically, the embodiments described herein relate to compositions containing polynucleotide molecules for altering the physiology of plants and modulating the effect of herbicide treatment. Further provided are methods and compositions useful for weed control.

BACKGROUND OF THE INVENTION

[0002] Weeds are plants that compete with cultivated plants in an agronomic environment and cost farmers billions of dollars annually in crop losses and the expense of efforts to keep weeds under control. Weeds also serve as hosts for crop diseases and insect pests. The losses caused by weeds in agricultural production environments include decreases in crop yield, reduced crop quality, increased irrigation costs, increased harvesting costs, reduced land value, injury to livestock, and crop damage from insects and diseases harbored by the weeds. The principal means by which weeds cause these effects are: 1) competing with crop plants for water, nutrients, sunlight and other essentials for growth and development, 2) production of toxic or irritant chemicals that cause human or animal health problem, 3) production of immense quantities of seed or vegetative reproductive parts or both that contaminate agricultural products and perpetuate the species in agricultural lands, and 4) production on agricultural and nonagricultural lands of vast amounts of vegetation that must be disposed of. Herbicide tolerant weeds are a problem with nearly all herbicides in use, there is a need to effectively manage these weeds. There are over 365 weed biotypes currently identified as being herbicide resistant to one or more herbicides by the Herbicide Resistance Action Committee (HRAC), the North American Herbicide Resistance Action Committee (NAHRAC), and the Weed Science Society of America (WSSA).

[0003] Plants have chloroplasts in which nuclear encoded proteins are imported. The import function is a key process related to the normal activity of the chloroplast. Genes associated with the chloroplast protein import and processing include but are not limited to the structural genes that encode for translocon at the outer envelope membrane of a chloroplast (Toc), a translocon at the inner envelope membrane of a chloroplast (Tic), a stroma processing peptidase (SPP) and chaperone like proteins associated with the chloroplast protein import system. The import of essential proteins into the chloroplast can be achieved by modulating the level of import proteins produced by the plants nuclear encoded genes. Many enzymes that are targets for herbicide action are nuclear encoded and imported into the chloroplast.

[0004] Embodiments of the present invention provide polynucleotide compositions useful for modulating gene expression in a plant, in particular, weedy plants for the purpose of enhancing control of the weeds in an agronomic environment and for the management of herbicide resistant weeds.

SUMMARY OF THE INVENTION

[0005] The present invention provides compositions for topical application to a surface of a plant comprising a polynucleotide and an organosilicone surfactant, wherein the polynucleotide is identical or complementary to at least 21 contiguous nucleotides of a sequence of a gene of the plant that encodes a polypeptide that is a component of a chloroplast protein import system selected from the group consisting of a translocon at the outer envelope membrane of a chloroplast (TOC), a translocon at the inner envelope membrane of a chloroplast (TIC), a stroma processing peptidase (SPP), and a chaperone like protein associated with the chloroplast protein import system, wherein the polynucleotide is selected from the group consisting of SEQ ID NOs: 1264-1583, 1639 and 1640, and upon a topical application of the composition to the surface of the plant, the composition suppresses the expression of the gene in the plant, thereby making the plant more sensitive to glyphosate, relative to a plant not treated with the polynucleotide.

[0006] These compositions may further comprise a pesticide, wherein said pesticide is selected from the group consisting of insecticides, fungicides, nematocides, bactericides, acaricides, growth regulators, chemosterilants, semiochemicals, repellents, attractants, pheromones, feeding stimulants, biopesticides and a combination thereof.

[0007] In a related embodiment the present invention provides methods of plant control comprising: topically applying to a surface of a plant a composition comprising a polynucleotide and an organosilicone surfactant, wherein the polynucleotide is identical or complementary to at least 21 contiguous nucleotides of a sequence of a gene of the plant that encodes a polypeptide that is a component of a chloroplast protein import system selected from the group consisting of a translocon at the outer envelope membrane of a chloroplast (TOC), a translocon at the inner envelope membrane of a chloroplast (TIC), a stroma processing peptidase (SPP), and a chaperone like protein associated with the chloroplast protein import system, wherein the polynucleotide is selected from the group consisting of SEQ ID NOs: 1264-1583, 1639 and 1640, and wherein the composition suppresses the expression of the gene in the plant, thereby making the plant more sensitive to glyphosate, relative to a plant not treated with the polynucleotide.

BRIEF DESCRIPTION OF THE FIGURES

[0008] The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. Embodiments described herein may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein. The present embodiments can be more fully understood from the following description of the figures:

Figure 1. Treatment of *Amaranthus palmeri* with dsRNA trigger polynucleotides targeting OEP80.

DETAILED DESCRIPTION

[0009] Provided are methods and compositions as described above containing a polynucleotide that provides for regulation and/or modulation of plant chloroplast protein import system or import processing enzyme genes,

[0010] Chloroplasts have to import more than 95 percent of their protein complement post-translationally from the cytosol. The vast majority of chloroplast proteins are synthesized as precursor proteins (preproteins) in the cytosol and are imported post-translationally into the organelle. Most proteins that are destined for the thylakoid membrane, the stroma and the inner envelope are synthesized with an amino-terminal extension called a presequence, or transit sequence, which is proteolytically removed after import. Preproteins that contain a cleavable transit peptide are recognized in a GTP-regulated manner by receptors of the outer-envelope translocon, which is called the TOC complex. The preproteins cross the outer envelope through an aqueous pore and are then transferred to the translocon in the inner envelope, which is called the TIC complex. The TOC and TIC translocons function together during the translocation process. Completion of import requires energy, which probably comes from the ATP-dependent functioning of molecular chaperones in the stroma. The stromal processing peptidase then cleaves the transit sequence to produce the mature form of the protein, which can fold into its native form. Plant gene polynucleotide sequences regulating the expression or encoding the enzymes involved in the chloroplast protein import system of target weed species are illustrated in SEQ ID NO: 1-1263 and SEQ ID NO: 1584-1638. Representative polynucleotide trigger molecules that are homologous or complementary to a segment of a chloroplast protein import system gene are illustrated in Table 2 (SEQ ID NO: 1264-1483), Table 3 (SEQ ID NO: 1483-1534), Table 5 (SEQ ID NO: 1535-1573) and Table 6 (SEQ ID NO: 1574-1583) and SEQ ID NO: 1639 and 1640. The treatment of plants with one or more of the trigger polynucleotides enhances plant sensitivity to one or more chemical herbicides.

[0011] Chloroplasts are critical organelles to the plant. Not only are they the centers for photosynthesis, but amino acids, lipid components and fatty acids of the cell membranes are synthesized by chloroplasts and they reduce nitrogen into ammonia and other organic compounds.

[0012] Aspects of the method can be applied to manage various weedy plants in agronomic and other cultivated environments.

[0013] The following definitions and methods are provided to better define the present invention and to guide those of ordinary skill in the art in the practice of the embodiments described herein. Unless otherwise noted, terms are to be understood according to conventional usage by those of ordinary skill in the relevant art. Where a term is provided in the singular, the inventors also contemplate aspects of the invention described by the plural of that term.

[0014] Weedy plants are plants that compete with cultivated plants, those of particular importance include, but are not limited to important invasive and noxious weeds and herbicide resistant biotypes in crop production, for example, *Amaranthus* species - *A. albus*, *A. blitoides*, *A. hybridus*, *A. palmeri*, *A. powellii*, *A. retroflexus*, *A. spinosus*, *A. tuberculatus*, and *A. viridis*; *Ambrosia* species - *A. trifida*, *A. artemisiifolia*; *Lolium* species - *L. multiflorum*, *L. rigidum*, *L. perenne*; *Digitaria* species - *D. insularis*; *Euphorbia* species - *E. heterophylla*; *Kochia* species - *K. scoparia*; *Sorghum* species - *S. halepense*; *Conyza* species - *C. bonariensis*, *C. canadensis*, *C. sumatrensis*; *Chloris* species - *C. truncate*; *Echinochloa* species - *E. colona*, *E. crus-galli*; *Eleusine* species - *E. indica*; *Poa* species - *P. annua*; *Plantago* species - *P. lanceolata*; *Avena* species - *A. fatua*; *Chenopodium* species - *C. album*; *Setaria* species - *S. viridis*; *Abutilon* species - *A. theophrasti*, *Ipomoea* species *Sesbania*, species, *Cassia* species, *Sida* species, *Brachiaria*, species and *Solanum* species.

[0015] Additional weedy plant species found in cultivated areas include *Alopecurus myosuroides*, *Avena sterilis*, *Avena sterilis ludoviciana*, *Brachiaria plantaginea*, *Bromus diandrus*, *Bromus rigidus*, *Cynosurus echinatus*, *Digitaria ciliaris*, *Digitaria ischaemum*, *Digitaria sanguinalis*, *Echinochloa oryzicola*, *Echinochloa phyllopogon*, *Eriochloa punctata*, *Hordeum glaucum*, *Hordeum leporinum*, *Ischaemum rugosum*, *Leptochloa chinensis*, *Lolium persicum*, *Phalaris minor*, *Phalaris paradoxa*, *Rottboellia exalta*, *Setaria faberi*, *Setaria viridis* var. *robusta-alba schreiber*, *Setaria viridis* var. *robusta-purpurea*, *Snowdenia polystachea*, *Sorghum sudanese*, *Alisma plantago-aquatica*, *Amaranthus lividus*, *Amaranthus quitensis*, *Ammania auriculata*, *Ammania coccinea*, *Anthemis cotula*, *Apera spica-venti*, *Bacopa rotundifolia*, *Bidens pilosa*, *Bidens subalternans*, *Brassica tournefortii*, *Bromus tectorum*, *Camelina microcarpa*, *Chrysanthemum coronarium*, *Cuscuta campestris*, *Cyperus difformis*, *Damasonium minus*, *Descurainia sophia*, *Diplotaxis tenuifolia*, *Echium plantagineum*, *Elatine triandra* var. *pedicellata*, *Euphorbia heterophylla*, *Fallopia convolvulus*, *Fimbristylis miliacea*, *Galeopsis*

tetrahit, *Galium spurium*, *Helianthus annuus*, *Iva xanthifolia*, *Ixophorus unisetus*, *Ipomoea indica*, *Ipomoea purpurea*, *Ipomoea sepiaria*, *Ipomoea aquatic*, *Ipomoea triloba*, *Lactuca serriola*, *Limnocharis flava*, *Limnophila erecta*, *Limnophila sessiliflora*, *Lindernia dubia*, *Lindernia dubia* var. *major*, *Lindernia micrantha*, *Lindernia procumbens*, *Mesembryanthemum crystallinum*, *Monochoria korsakowii*, *Monochoria vaginalis*, *Neslia paniculata*, *Papaver rhoeas*, *Parthenium hysterophorus*, *Pentzia suffruticosa*, *Phalaris minor*, *Raphanus raphanistrum*, *Raphanus sativus*, *Rapistrum rugosum*, *Rotala indica* var. *uliginosa*, *Sagittaria guyanensis*, *Sagittaria montevidensis*, *Sagittaria pygmaea*, *Salsola iberica*, *Scirpus juncooides* var. *ohwianus*, *Scirpus mucronatus*, *Setaria lutescens*, *Sida spinosa*, *Sinapis arvensis*, *Sisymbrium orientale*, *Sisymbrium thellungii*, *Solanum ptycanthum*, *Sonchus asper*, *Sonchus oleraceus*, *Sorghum bicolor*, *Stellaria media*, *Thlaspi arvense*, *Xanthium strumarium*, *Arctotheca calendula*, *Conyza sumatrensis*, *Crassocephalum crepidioides*, *Cuphea carthagenensis*, *Epilobium adenocaulon*, *Erigeron philadelphicus*, *Landoltia punctata*, *Lepidium virginicum*, *Monochoria korsakowii*, *Solanum americanum*, *Solanum nigrum*, *Vulpia bromoides*, *Youngia japonica*, *Hydrilla verticillata*, *Carduus nutans*, *Carduus pycnocephalus*, *Centaurea solstitialis*, *Cirsium arvense*, *Commelina diffusa*, *Convolvulus arvensis*, *Daucus carota*, *Digitaria ischaemum*, *Echinochloa crus-galli*, *Fimbristylis miliacea*, *Galeopsis tetrahit*, *Galium spurium*, *Limnophila erecta*, *Matricaria perforata*, *Papaver rhoeas*, *Ranunculus acris*, *Soliva sessilis*, *Sphenoclea zeylanica*, *Stellaria media*, *Nassella trichotoma*, *Stipa neesiana*, *Agrostis stolonifera*, *Polygonum aviculare*, *Alopecurus japonicus*, *Beckmannia syzigachne*, *Bromus tectorum*, *Chloris inflata*, *Echinochloa erecta*, *Portulaca oleracea*, and *Senecio vulgaris*. All plants contain chloroplast import protein system genes, the sequence of which can be isolated and polynucleotides selected according to the methods described herein that are useful for altering the physiology of the plant and making the plant more sensitive to a herbicide.

[0016] Numerous chemical herbicide, herein referred to as nonpolynucleotide herbicides, are available that can be added to a composition as described herein that provide multi-species weed control or alternative modes of action for difficult to control weed species, for example, members of the herbicide families that include but are not limited to 1,5-Diarylpyrazole herbicides, 2-Thiopyrimidine herbicides, 3-CF₃-Benzene herbicides, Acetamide herbicides, Amide herbicides, Aminoacrylate herbicides, Aminotriazine herbicides, Aromatic acid herbicides, Arsenical herbicides, Arylamino-propionic acid herbicides, Arylcarboxamide herbicides, Arylcyclodione herbicides, Aryloxyphenoxy-propionate herbicides, Azolecarboxamide herbicides, Azoloazinone herbicides, Azolotriazine herbicides, Benzamide herbicides, Benzenesulfonamide herbicides, Benzhydryl herbicides, Benzimidazole herbicides, Benzofuran herbicides, Benzofuranyl Alkylsulfonate herbicides, Benzohydrazide herbicides, Benzoic acid herbicides, Benzophenylmethanone herbicides, Benzothiadiazinone herbicides, Benzothiazole herbicides, Benzothiazoleacetate herbicides, Benzoxazole herbicides, Benzoylcyclohexanedione herbicides, Benzyloxymethylisoxazole herbicides, Benzylpyrazole herbicides, Benzylpyridine herbicides, Benzylpyrimidone herbicides, Bipyridylum herbicides, Carbamate herbicides, Chloroacetamide herbicides, Chloroacetamide herbicides, Chlorocarbonic acid herbicides, Cyclohexanedione herbicides, Cyclohexene oxime herbicides, Cyclopropylisoxazole herbicides, Diarylether herbicides, Dicarboximide herbicides, Dihydropyranocarboxamide herbicides, Diketo-epoxide herbicides, Diketopiperazine herbicides, Dinitroaniline herbicides, Dinitrophenol herbicides, Diphenylether herbicides, Diphenylfuranone herbicides, Dithiocarbamate herbicides, Fluoroalkene herbicides, Glyphosate herbicides, Halogenated aliphatic herbicides, Hydantocidin herbicides, Hydroxypyrazole herbicides, Imidazolinone herbicides, Indazole herbicides, Indenedione herbicides, Inorganic herbicides, Isoxazole herbicides, Isoxazolesulfone herbicides, Isoxazolidinone herbicides, Nicotinohydrazide herbicides, Nitrile herbicides, Nitrile-amide herbicides, Nitro-pyrazole herbicides, N-phenylphthalimide herbicides, Organoarsenical herbicides, Organophosphates herbicides, Organophosphorus herbicides, Oxabicycloheptane herbicides, Oxadiazole herbicides, Oxadiazolebenzamide herbicides, Oxadiazolone herbicides, Oxazole herbicides, Oxazolidinedione herbicides, Oxyacetamide herbicides, Phenoxy herbicides, Phenoxyalkyne herbicides, Phenoxycarboxylic acid herbicides, Phenoxy-pyridazinol herbicides, Phenylalkanoate herbicides, Phenylcarbamate herbicides, Phenylenediamine herbicides, Phenylethylurea herbicides, Phenylimidazole herbicides, Phenylisoxazole herbicides, Phenylpyrazole herbicides, Phenylpyrazoline herbicides, Phenylpyridazine herbicides, Phenylpyridine herbicides, Phenylpyrrolidone herbicides, Phosphinic acid herbicides, Phosphonate herbicides, Phosphoroamidate herbicides, Phosphorodithioate herbicides, Phthalamate herbicides, Propionamide herbicides, Pyrazole herbicides, Pyrazole-arylether herbicides, Pyrazolium herbicides, Pyridazine herbicides, Pyridazinone herbicides, Pyridine herbicides, Pyridinecarboxamide herbicides, Pyridinecarboxylic acid herbicides, Pyridinone herbicides, Pyridylbenzylamide herbicides, Pyridyl-ether-carboxamide herbicides, Pyrimidinecarboxylic acid herbicides, Pyrimidinediamine herbicides, Pyrimidinedione herbicides, Pyrimidinetrione herbicides, Pyrimidinone herbicides, Pyrimidinyl(thio)benzoate herbicides, Pyrimidinyl-oxymethylamine herbicides, Pyrimidylmethanol herbicides, Pyrrolidone herbicides, Quaternary Ammonium herbicides, Quinoline-carboxylic acid herbicides, Quinoxaline herbicides, Semicarbazone herbicides, Sulfonamide herbicides, Sulfonylamino-carbonyl-triazolinone herbicides, Sulfonylurea herbicides, Sulfonylurea herbicides, Tetrazolinone herbicides, Thiadiazole herbicides, Thiatriazine herbicides, Thienopyrimidine herbicides, Thiocarbamate herbicides, Thiocarbonate herbicides, Thiourea herbicides, Tolyltriazole herbicides, Triazine herbicides, Triazinedione herbicides, Triazine-sulfonanilide herbicides, Triazinone herbicides, Triazole herbicides, Triazolecarboxamide herbicides, Triazoleimine herbicides, Triazolinone herbicides, Triazolone herbicides, Triazolopyrimidine herbicides, Triketone herbicides, Uracil herbicides, and Urea herbicides. In particular, the rates of use of the added herbicides can be reduced

in compositions comprising polynucleotides as described herein. Use rate reductions of the additional added herbicides can be 10-25 percent, 26-50 percent, 51-75 percent or more can be achieved that enhance the activity of the polynucleotides and herbicide composition and is contemplated as an aspect of the invention.

[0017] Additional herbicidal compounds of unspecified modes of action as described in CN101279950A, CN101279951A, DE10000600A1, DE10116399A1, DE102004054666A1, DE102005014638A1, DE102005014906A1, DE102007012168A1, DE102010042866A1, DE10204951A1, DE10234875A1, DE10234876A1, DE10256353A1, DE10256354A1, DE10256367A1, EP1157991A2, EP1238586A1, EP2147919A1, EP2160098A2, JP03968012B2, JP2001253874A, JP2002080454A, JP2002138075A, JP2002145707A, JP2002220389A, JP2003064059A, JP2003096059A, JP2004051628A, JP2004107228A, JP2005008583A, JP2005239675A, JP2005314407A, JP2006232824A, JP2006282552A, JP2007153847A, JP2007161701A, JP2007182404A, JP2008074840A, JP2008074841A, JP2008133207A, JP2008133218A, JP2008169121A, JP2009067739A, JP2009114128A, JP2009126792A, JP2009137851A, US20060111241A1, US20090036311A1, US20090054240A1, US20090215628A1, US20100099561A1, US20100152443A1, US20110105329A1, US20110201501A1, WO2001055066A2, WO2001056975A1, WO2001056979A1, WO2001090071A2, WO2001090080A1, WO2002002540A1, WO2002028182A1, WO2002040473A1, WO2002044173A2, WO2003000679A2, WO2003006422A1, WO2003013247A1, WO2003016308A1, WO2003020704A1, WO2003022051A1, WO2003022831A1, WO2003022843A1, WO2003029243A2, WO2003037085A1, WO2003037878A1, WO2003045878A2, WO2003050087A2, WO2003051823A1, WO2003051824A1, WO2003051846A2, WO2003076409A1, WO2003087067A1, WO2003090539A1, WO2003091217A1, WO2003093269A2, WO2003104206A2, WO2004002947A1, WO2004002981A2, WO2004011429A1, WO2004029060A1, WO2004035545A2, WO2004035563A1, WO2004035564A1, WO2004037787A1, WO2004067518A1, WO2004067527A1, WO2004077950A1, WO2005000824A1, WO2005007627A1, WO2005040152A1, WO2005047233A1, WO2005047281A1, WO2005061443A2, WO2005061464A1, WO2005068434A1, WO2005070889A1, WO2005089551A1, WO2005095335A1, WO2006006569A1, WO2006024820A1, WO2006029828A1, WO2006029829A1, WO2006037945A1, WO2006050803A1, WO2006090792A1, WO2006123088A2, WO2006125687A1, WO2006125688A1, WO2007003294A1, WO2007026834A1, WO2007071900A1, WO2007077201A1, WO2007077247A1, WO2007096576A1, WO2007119434A1, WO2007134984A1, WO2008009908A1, WO2008029084A1, WO2008059948A1, WO2008071918A1, WO2008074991A1, WO2008084073A1, WO2008100426A2, WO2008102908A1, WO2008152072A2, WO2008152073A2, WO2009000757A1, WO2009005297A2, WO2009035150A2, WO2009063180A1, WO2009068170A2, WO2009068171A2, WO2009086041A1, WO2009090401A2, WO2009090402A2, WO2009115788A1, WO2009116558A1, WO2009152995A1, WO2009158258A1, WO2010012649A1, WO2010012649A1, WO2010026989A1, WO2010034153A1, WO2010049270A1, WO2010049369A1, WO2010049405A1, WO2010049414A1, WO2010063422A1, WO2010069802A1, WO2010078906A2, WO2010078912A1, WO2010104217A1, WO2010108611A1, WO2010112826A3, WO2010116122A3, WO2010119906A1, WO2010130970A1, WO2011003776A2, WO2011035874A1, WO2011065451A1, are useful to include in combination with polynucleotides targeting the plant chloroplast import protein or import processing enzyme genes.

[0018] In some embodiments, a composition includes a nonpolynucleotide herbicide component such as glyphosate (N-phosphonomethylglycine) herbicide inhibits the shikimic acid pathway which leads to the biosynthesis of aromatic compounds including amino acids, plant hormones and vitamins. Specifically, glyphosate curbs the conversion of phosphoenolpyruvic acid (PEP) and 3-phosphoshikimic acid to 5-enolpyruvyl-3-phosphoshikimic acid by inhibiting the enzyme 5-enolpyruvylshikimate-3-phosphate synthase (hereinafter referred to as EPSP synthase or EPSPS). For purposes of the present embodiments, the term "glyphosate" should be considered to include any herbicidally effective form of N-phosphonomethylglycine (including any salt thereof) and other forms which result in the production of the glyphosate anion in planta. Glyphosate is an example of an EPSPS inhibitor herbicide. Herbicides are molecules that affect plant growth or development or reproductive ability. Glyphosate is commercially available in numerous formulations. Examples of these formulations of glyphosate include, without limitation, those sold by Monsanto Company (St Louis, MO) as ROUNDUP®, ROUNDUP® ULTRA,

ROUNDUP®ULTRAMAX, ROUNDUP®CT, ROUNDUP®EXTRA, ROUNDUP®BIACTIVE, ROUNDUP®BIOFORCE, RODEO®, POLARIS®, SPARK® and

[0019] ACCORD® herbicides, all of which contain glyphosate as its isopropylammonium salt, ROUNDUP® WEATHERMAX containing glyphosate as its potassium salt; ROUNDUP® DRY and RIVAL® herbicides, which contain glyphosate as its ammonium salt; ROUNDUP® GEOFORCE, which contains glyphosate as its sodium salt; and TOUCHDOWN® herbicide (Syngenta, Greensboro, NC), which contains glyphosate as its trimethylsulfonium salt or monopotassium salt. Various other salts of glyphosate are available for example, dimethylamine salt, isopropylamine salt, trimesium salt,

potassium salt, monoammonium salt, and diammonium salt.

[0020] In some embodiments, a composition may include a nonpolynucleotide herbicide component that is an acetolactate synthase (ALS) inhibitor herbicide which includes but are not limited to amidosulfuron, azimsulfuron, bensulfuron-methyl, chlorimuron-ethyl, chlorsulfuron, cinosulfuron, cyclosulfamuron, ethametsulfuron-methyl, ethoxysulfuron, flazasulfuron, flupyrsulfuron-methyl-Na, foramsulfuron, halosulfuron-methyl, imazosulfuron, iodosulfuron, metsulfuron-methyl, nicosulfuron, oxasulfuron, primisulfuron-methyl, prosulfuron, pyrazosulfuron-ethyl, rimsulfuron, sulfometuron-methyl, sulfosulfuron, thifensulfuron-methyl, triasulfuron, tribenuron-methyl, trifloxysulfuron, triflurosulfuron-methyl, tritosulfuron, imazapic, imazamethabenz-methyl, imazamox, imazapyr, imazaquin, imazethapyr, cloransulam-methyl, diclosulam, florasulam, flumetsulam, metosulam, bispyribac-Na, pyribenzoxim, pyriftalid, pyriothiac-Na, pyriminobac-methyl, flucarbazone-Na, and procarbazone-Na.

[0021] In some embodiments, a composition may include a nonpolynucleotide herbicide component that is an acetyl-CoA carboxylase (ACCase) inhibitor herbicide, which include members of the chemical families of aryloxyphenoxypropionates, cyclohexanediones and phenylpyrazoline that include, but are not limited to an aryloxyphenoxypropionate comprising clodinafop (Propanoic acid, 2-[4-[(5-chloro-3-fluoro-2-pyridinyl)oxy]phenoxy]-2-propynyl ester, (2R)), cyhalofop (butyl(2R)-2-[4-(4-cyano-2-fluorophenoxy)phenoxy] propionate), diclofop (methyl 2-[4-(2,4-dichlorophenoxy)phenoxy]propanoate), fenoxaprop (ethyl (R)-2-[4-(6-chloro-1,3-benzoxazol-2-yloxy)phenoxy]propionate), fluazifop (2R)-2-[4-[[5-(trifluoromethyl)-2-pyridinyl]oxy]phenoxy]propanoic acid), haloxyfop (2-[4-[[3-chloro-5-(trifluoromethyl)-2-pyridinyl]oxy]phenoxy]propanoic acid), propaquizafop (2-[[[1-methylethylidene]amino]oxy]ethyl (2R)-2-[4-[(6-chloro-2-quinoxalinyloxy]phenoxy]propanoate) and quizalofop(2R)-2-[4-[(6-chloro-2-quinoxalinyloxy]phenoxy]propanoic acid; a cyclohexanedione comprising alloxydim (methyl 2,2-dimethyl-4,6-dioxo-5-[(1E)-1-[(2-propen-1-yloxy)imino]butyl]cyclohexanecarboxylate), butoxydim (2-[1-(ethoxyimino)propyl]-3-hydroxy-5-[2,4,6-trimethyl-3-(1-oxobutyl)phenyl]-2-cyclohexen-1-one), clethodim (2-[1-[[[(2E)-3-chloro-2-propen-1-yl]oxy]imino]propyl]-5-[2-(ethylthio)propyl]-3-hydroxy-2-cyclohexen-1-one), cycloxydim (2-[1-(ethoxyimino)butyl]-3-hydroxy-5-(tetrahydro-2H-thiopyran-3-yl)-2-cyclohexen-1-one), profoxydim (2-[1-[[2-(4-chlorophenoxy)propoxy]imino]butyl]-3-hydroxy-5-(tetrahydro-2H-thiopyran-3-yl)-2-cyclohexen-1-one), sethoxydim (2-[1-(ethoxyimino)butyl]-5-[2-(ethylthio)propyl]-3-hydroxy-2-cyclohexen-1-one), tepraloxym (2-[1-[[[(2E)-3-chloro-2-propen-1-yl]oxy]imino]propyl]-3-hydroxy-5-(tetrahydro-2H-pyran-4-yl)-2-cyclohexen-1-one) and tralkoxydim (2-[1-(ethoxyimino)propyl]-3-hydroxy-5-(2,4,6-trimethylphenyl)-2-cyclohexen-1-one); a phenylpyrazoline comprising pinoxaden (8-(2,6-diethyl-4-methylphenyl)-1,2,4,5-tetrahydro-7-oxo-7H-pyrazolo[1,2-d][1,4,5]oxadiazepin-9-yl-2,2-dimethylpropanoate).

[0022] In some embodiments, a composition may include a nonpolynucleotide herbicide component that is an -hydroxyphenyl-pyruvate-dioxygenase (HPPD) inhibitor herbicide which includes but are not limited to Triketones, such as, mesotrione, tefuryltrione, tembotrione, and sulcotrione; Isoxazoles, such as, isoxachlortole, pyrasulfotole, and isoxaflutole; Pyrazoles, such as, benzofenap, pyrazolynate, topramezone and pyrazoxyfen. Additional HPPD inhibitors include benzobicyclon and bicyclopypyrone,

[0023] In some embodiments, a composition may include a nonpolynucleotide herbicide component that is a glutamine synthetase (GS) inhibitor herbicide, which include members of the Phosphinic acids herbicide group such as glufosinate-ammonium and bialaphos.

[0024] In some embodiments, a composition may include a nonpolynucleotide herbicide component that is an phytoene desaturase (PDS) inhibitor herbicide, which include but are not limited to norflurazon, diflufenican, picolinafen, beflubutamid, fluridone, flurochloridone and flurtamone.

[0025] In some embodiments, a composition may include a nonpolynucleotide herbicide component that is an protoporphyrinogen IX oxidase (PPG oxidase) inhibitor herbicide, which include but are not limited to acifluorfen-Na, bifenox, chlormethoxyfen, fluoroglycofen-ethyl, fomesafen, halosafen, lactofen, oxyfluorfen, fluazolate, pyraflufen-ethyl, cinidon-ethyl, flumioxazin, flumiclorac-pentyl, fluthiacet-methyl, thidiazimin, oxadiazon, oxadiargyl, azafenidin, carfentrazone-ethyl, sulfentrazone, pentoxazone, benzfendazole, butafenacil, pyrazogyl, and proflumazone.

[0026] In some embodiments, a composition may include a nonpolynucleotide herbicide component that is dihydropyran synthetase (DHPS) inhibitor herbicides include but are not limited to sulfonamides and asulam.

[0027] In some embodiments, a composition may include a nonpolynucleotide herbicide component that is photosystem II D1 protein (psbA) inhibitor herbicides include but are not limited to the chemical families of Triazines, Triazinones, Triazolinone, Uracils, Pyridazinones, Phenyl-carbamates, Ureas, Amides, Nitriles, Benzothiadiazinone, Phenyl-pyridazines and include members such as diuron [3-(3,4-dichlorophenyl)-1,1-dimethylurea], chlortoluron, isoproturon, linuron, tebuthiuron, bentazone, oxadiazon, bromacil, ametryne, atrazine, cyanazine, hexazinone, metribuzin, simazine, and terbutylazine.

[0028] An agronomic field in need of plant control is treated by application of a composition as described herein directly to the surface of the growing plants, such as by a spray. For example, the method is applied to control weeds in a field of crop plants by spraying the field with the composition. The composition can be provided as a tank mix, a sequential treatment of components, or a simultaneous treatment or mixing of one or more of the components of the composition from separate containers. Treatment of the field can occur as often as needed to provide weed control and the components

of the composition can be adjusted to target specific weed species or weed families through utilization of specific polynucleotides or polynucleotide compositions capable of selectively targeting the specific species or plant family to be controlled. The composition can be applied at effective use rates according to the time of application to the field, for example, preplant, at planting, post planting, post-harvest. Herbicide components of the composition can be applied at manufacturer's recommended use rates or reduced use rates, for example, 10-25 percent, or 26-50 percent, or 51-75 percent of the recommend use rate. The polynucleotides of the composition can be applied at rates of 1 to 30 grams per acre depending on the number of trigger molecules needed for the scope of weeds in the field.

[0029] Crop plants in which weed control may be needed include but are not limited to corn, soybean, cotton, canola, sugar beet, alfalfa, sugarcane, rice, and wheat; vegetable plants including, but not limited to, tomato, sweet pepper, hot pepper, melon, watermelon, cucumber, eggplant, cauliflower, broccoli, lettuce, spinach, onion, peas, carrots, sweet corn, Chinese cabbage, leek, fennel, pumpkin, squash or gourd, radish, Brussels sprouts, tomatillo, garden beans, dry beans, or okra; culinary plants including, but not limited to, basil, parsley, coffee, or tea; or fruit plants including but not limited to apple, pear, cherry, peach, plum, apricot, banana, plantain, oil palm, rubber tree, table grape, wine grape, citrus, avocado, mango, or berry; a tree grown for ornamental or commercial use, including, but not limited to, a fruit or nut tree; ornamental plant (e. g., an ornamental flowering plant or shrub or turf grass). The methods and compositions provided herein can also be applied to plants produced by a cutting, cloning, or grafting process (i.e., a plant not grown from a seed) including fruit trees and plants that include, but are not limited to, avocados, tomatoes, eggplant, cucumber, melons, watermelons, and grapes as well as various ornamental plants.

Polynucleotides

[0030] As used herein, the term "DNA", "DNA molecule", "DNA polynucleotide molecule" refers to a single-stranded DNA (ssDNA) or double-stranded DNA (dsDNA) molecule of genomic or synthetic origin, such as, a polymer of deoxyribonucleotide bases or a DNA polynucleotide molecule. As used herein, the term "DNA sequence", "DNA nucleotide sequence" or "DNA polynucleotide sequence" refers to the nucleotide sequence of a DNA molecule. As used herein, the term "RNA", "RNA molecule", "RNA polynucleotide molecule" refers to a single-stranded RNA (ssRNA) or double-stranded RNA (dsRNA) molecule of genomic or synthetic origin, such as, a polymer of ribonucleotide bases that comprise single or double stranded regions. Unless otherwise stated, nucleotide sequences in the text of this specification are given, when read from left to right, in the 5' to 3' direction and generally represent the plus or sense strand of a double strand polynucleotide. It is recognized that the minus or antisense strand may be the functional moiety of a double strand polynucleotide in the present embodiments although unless indicate the disclosed polynucleotide sequences will represent the plus or sense strand polynucleotide sequence. The nomenclature used herein is that required by Title 37 of the United States Code of Federal Regulations § 1.822 and set forth in the tables in WIPO Standard ST.25 (1998), Appendix 2, Tables 1, 2, and 3.

[0031] As used herein, "polynucleotide" refers to a DNA or RNA molecule containing multiple nucleotides and generally refers both to "oligonucleotides" (a polynucleotide molecule of typically 50 or fewer nucleotides in length) and polynucleotides of 51 or more nucleotides. Embodiments include compositions including oligonucleotides having a length of at least 21 nucleotides (21-mers, 22-mers, 23-mers, 24-mers, or 25-mers), for example, oligonucleotides essentially identical or complementary to a component of a chloroplast protein import system as described above. Where a polynucleotide is double-stranded, its length can be similarly described in terms of base pairs. A target gene comprises any polynucleotide molecule in a plant cell or fragment thereof for which the modulation of the expression of the target gene is provided by the methods and compositions. A gene has noncoding genetic elements (components) that provide for the function of the gene, these elements are polynucleotides that provide gene expression regulation, such as, a promoter, an enhancer, a 5' untranslated region, intron regions, and a 3' untranslated region. Oligonucleotides and polynucleotides can be made to any of the genetic elements of a gene and to polynucleotides spanning the junction region of a genetic element, such as, an intron and exon, the junction region of a promoter and a transcribed region, the junction region of a 5' leader and a coding sequence, the junction of a 3' untranslated region and a coding sequence.

[0032] Polynucleotide compositions used in the various embodiments include compositions including polynucleotides as described above.

[0033] The polynucleotides can be single- or double-stranded RNA or single- or double-stranded DNA or double-stranded DNA/RNA hybrids or modified analogues thereof, and can be of oligonucleotide lengths or longer. In more specific embodiments, the polynucleotides that provide single-stranded RNA in the plant cell are selected from the group consisting of (a) a single-stranded RNA molecule (ssRNA), (b) a single-stranded RNA molecule that self-hybridizes to form a double-stranded RNA molecule, (c) a double-stranded RNA molecule (dsRNA), (d) a single-stranded DNA molecule (ssDNA), (e) a single-stranded DNA molecule that self-hybridizes to form a double-stranded DNA molecule, and (f) a single-stranded DNA molecule including a modified Pol III gene that is transcribed to an RNA molecule, (g) a double-stranded DNA molecule (dsDNA), (h) a double-stranded DNA molecule including a modified Pol III gene that is transcribed to an RNA molecule, (i) a double-stranded, hybridized RNA/DNA molecule, or combinations thereof. some embodiments,

the oligonucleotides may be blunt-ended or may comprise a 3' overhang of from 1-5 nucleotides of at least one or both of the strands. Other configurations of the oligonucleotide are known in the field and are contemplated herein. In embodiments of the method the polynucleotides include double-stranded DNA formed by intramolecular hybridization, double-stranded DNA formed by intermolecular hybridization, double-stranded RNA formed by intramolecular hybridization, or double-stranded RNA formed by intermolecular hybridization. In one embodiment the polynucleotides include single-stranded DNA or single-stranded RNA that self-hybridizes to form a hairpin structure having an at least partially double-stranded structure including at least one segment that will hybridize to RNA transcribed from the gene targeted for suppression. Not intending to be bound by any mechanism, it is believed that such polynucleotides are or will produce single-stranded RNA with at least one segment that will hybridize to RNA transcribed from the gene targeted for suppression.

[0034] The term "gene" refers to components that comprise chromosomal DNA, plasmid DNA, cDNA, intron and exon DNA, artificial DNA polynucleotide, or other DNA that encodes a peptide, polypeptide, protein, or RNA transcript molecule, and the genetic elements flanking the coding sequence that are involved in the regulation of expression, such as, promoter regions, 5' leader regions, 3' untranslated region that may exist as native genes or transgenes in a plant genome. A component of a gene or a fragment thereof of a component of a chloroplast protein import system is isolated and subjected to polynucleotide sequencing methods that determines the order of the nucleotides that comprise the gene. Any of the components of the gene are potential targets for a trigger oligonucleotide and polynucleotides.

[0035] The trigger polynucleotide molecules are designed to modulate expression by inducing regulation or suppression of an endogenous chloroplast import protein system gene in a plant and are designed to have a nucleotide sequence essentially identical or essentially complementary to the nucleotide sequence of an endogenous chloroplast import protein system gene of a plant or to the sequence of RNA transcribed from an endogenous chloroplast import protein or import processing enzyme or chaperone like protein associated with the import protein system gene of a plant, the sequence thereof determined by isolating the gene or a fragment of the gene from the plant, which can be coding sequence or non-coding sequence. Effective molecules that modulate expression are referred to as "a trigger molecule, or trigger polynucleotide". By "essentially identical" or "essentially complementary" is meant that the trigger polynucleotides (or at least one strand of a double-stranded polynucleotide or portion thereof, or a portion of a single strand polynucleotide) are designed to hybridize to the endogenous gene noncoding sequence or to RNA transcribed (known as messenger RNA or an RNA transcript) from the endogenous gene to effect regulation or suppression of expression of the endogenous gene. Trigger molecules are identified by "tiling" the gene targets with partially overlapping probes or non-overlapping probes of antisense or sense polynucleotides that are essentially identical or essentially complementary to the nucleotide sequence of an endogenous gene. Multiple target sequences can be aligned and sequence regions with homology in common, according to the methods, are identified as potential trigger molecules for the multiple targets. Multiple trigger molecules of various lengths, for example 19-25 nucleotides, 26-40 nucleotides, 41-50 nucleotides, 51-59 nucleotides, 60-100 nucleotides, 101-200 nucleotides, 201-300 nucleotides or more can be pooled into a few treatments in order to investigate polynucleotide molecules that cover a portion of a gene sequence (for example, a portion of a coding versus a portion of a noncoding region, or a 5' versus a 3' portion of a gene) or an entire gene sequence including coding and noncoding regions of a target gene. Polynucleotide molecules of the pooled trigger molecules can be divided into smaller pools or single molecules in order to identify trigger molecules that provide the desired effect.

[0036] The target gene RNA and DNA polynucleotide molecules (SEQ ID NO:1-1263 and 1584-1638) are sequenced by any number of available methods and equipment. Some of the sequencing technologies are available commercially, such as the sequencing-by-hybridization platform from Affymetrix Inc. (Sunnyvale, Calif.) and the sequencing-by-synthesis platforms from 454 Life Sciences (Bradford, Conn.), Illumina/Solexa (Hayward, Calif.) and Helicos Biosciences (Cambridge, Mass.), and the sequencing-by-ligation platform from Applied Biosystems (Foster City, Calif.), as described below. In addition to the single molecule sequencing performed using sequencing-by-synthesis of Helicos Biosciences, other single molecule sequencing technologies are encompassed and include the SMRT™ technology of Pacific Biosciences, the Ion Torrent™ technology, and nanopore sequencing being developed for example, by Oxford Nanopore Technologies. A chloroplast import protein system or import processing enzyme gene comprising DNA or RNA can be isolated using primers or probes essentially complementary or essentially homologous to SEQ ID NO:1-1263 and 1584-1638 or a fragment thereof. A polymerase chain reaction (PCR) gene fragment can be produced using primers essentially complementary or essentially homologous to SEQ ID NO:1-1263 and 1584-1638 or a fragment thereof that is useful to isolate a chloroplast import protein or import processing enzyme gene from a plant genome. SEQ ID NO: 1-1263 and 1584-1638 or fragments thereof can be used in various sequence capture technologies to isolate additional target gene sequences, for example, including but not limited to Roche NimbleGen® (Madison, WI) and Streptavidin-coupled Dynabeads® (Life Technologies, Grand Island, NY) and US20110015084.

[0037] "Identity" refers to the degree of similarity between two polynucleic acid or protein sequences. An alignment of the two sequences is performed by a suitable computer program. A widely used and accepted computer program for performing sequence alignments is CLUSTALW v1.6 (Thompson, et al. Nucl. Acids Res., 22: 4673-4680, 1994). The

number of matching bases or amino acids is divided by the total number of bases or amino acids, and multiplied by 100 to obtain a percent identity. For example, if two 580 base pair sequences had 145 matched bases, they would be 25 percent identical. If the two compared sequences are of different lengths, the number of matches is divided by the shorter of the two lengths. For example, if there are 100 matched amino acids between a 200 and a 400 amino acid protein, they are 50 percent identical with respect to the shorter sequence. If the shorter sequence is less than 150 bases or 50 amino acids in length, the number of matches are divided by 150 (for nucleic acid bases) or 50 (for amino acids), and multiplied by 100 to obtain a percent identity.

[0038] Trigger molecules for specific gene family members can be identified from coding and/or non-coding sequences of gene families of a plant or multiple plants, by aligning and selecting 200-300 polynucleotide fragments from the least homologous regions amongst the aligned sequences and evaluated using topically applied polynucleotides (as sense or antisense ssDNA or ssRNA, dsRNA, or dsDNA) to determine their relative effectiveness in providing the herbicidal phenotype. The effective segments are further subdivided into 50-60 polynucleotide fragments, prioritized by least homology, and reevaluated using topically applied polynucleotides. In some embodiments, the effective 50-60 polynucleotide fragments are further subdivided into 19-30 polynucleotide fragments, prioritized by least homology, and again evaluated for induction of the herbicidal phenotype. Once relative effectiveness is determined, the fragments are utilized singly, or again evaluated in combination with one or more other fragments to determine the trigger composition or mixture of trigger polynucleotides for providing the herbicidal phenotype.

[0039] Trigger molecules for broad activity can be identified from coding and/or non-coding sequences of gene families of a plant or multiple plants, by aligning and selecting 200-300 polynucleotide fragments from the most homologous regions amongst the aligned sequences and evaluated using topically applied polynucleotides (as sense or anti-sense ssDNA or ssRNA, dsRNA, or dsDNA) to determine their relative effectiveness in inducing the herbicidal phenotype. The effective segments are subdivided into 50-60 polynucleotide fragments, prioritized by most homology, and reevaluated using topically applied polynucleotides. In some embodiments, effective 50-60 polynucleotide fragments are utilized singly, or in combination with one or more other fragments to determine the trigger composition or mixture of trigger polynucleotides for providing the herbicidal phenotype. In some embodiments, the effective 50-60 polynucleotide fragments are subdivided into 19-30 polynucleotide fragments, prioritized by most homology, and again evaluated for induction of the herbicidal phenotype. Once relative effectiveness is determined, the fragments may be utilized singly, or in combination with one or more other fragments to determine the trigger composition or mixture of trigger polynucleotides for providing the herbicidal phenotype.

[0040] Methods of making polynucleotides are well known in the art. Chemical synthesis, in vivo synthesis and in vitro synthesis methods and compositions are known in the art and include various viral elements, microbial cells, modified polymerases, and modified nucleotides. Commercial preparation of oligonucleotides often provides two deoxyribonucleotides on the 3' end of the sense strand. Long polynucleotide molecules can be synthesized from commercially available kits, for example, kits from Applied Biosystems/Ambion (Austin, TX) have DNA ligated on the 5' end in a microbial expression cassette that includes a bacterial T7 polymerase promoter that makes RNA strands that can be assembled into a dsRNA and kits provided by various manufacturers that include T7 RiboMax Express (Promega, Madison, WI), AmpliScribe T7-Flash (Epicentre, Madison, WI), and TranscriptAid T7 High Yield (Fermentas, Glen Burnie, MD). dsRNA molecules can be produced from microbial expression cassettes in bacterial cells (Ongvarrasopone et al. ScienceAsia 33:35-39; Yin, Appl. Microbiol. Biotechnol 84:323-333, 2009; Liu et al., BMC Biotechnology 10:85, 2010) that have regulated or deficient RNase III enzyme activity or the use of various viral vectors to produce sufficient quantities of dsRNA. Chloroplast import protein or import processing enzyme gene fragments are inserted into the microbial expression cassettes in a position in which the fragments are expressed to produce ssRNA or dsRNA useful in the methods described herein to regulate expression of a target gene. Long polynucleotide molecules can also be assembled from multiple RNA or DNA fragments. In some embodiments design parameters such as Reynolds score (Reynolds et al. Nature Biotechnology 22, 326 - 330 (2004), Tuschl rules (Pei and Tuschl, Nature Methods 3(9): 670-676, 2006), i-score (Nucleic Acids Res 35: e123, 2007), i-Score Designer tool and associated algorithms (Nucleic Acids Res 32: 936-948, 2004. Biochem Biophys Res Commun 316: 1050-1058, 2004, Nucleic Acids Res 32: 893-901, 2004, Cell Cycle 3: 790-5, 2004, Nat Biotechnol 23: 995-1001, 2005, Nucleic Acids Res 35: e27, 2007, BMC Bioinformatics 7: 520, 2006, Nucleic Acids Res 35: e123, 2007, Nat Biotechnol 22: 326-330, 2004) are known in the art and may be used in selecting polynucleotide sequences effective in gene silencing. In some embodiments the sequence of a polynucleotide is screened against the genomic DNA of the intended plant to minimize unintentional silencing of other genes.

[0041] Ligands can be tethered to a polynucleotide, for example a dsRNA, ssRNA, dsDNA or ssDNA. Ligands in general can include modifiers, e.g., for enhancing uptake; diagnostic compounds or reporter groups e.g., for monitoring distribution; cross-linking agents; nuclease-resistance conferring moieties; and natural or unusual nucleobases. General examples include lipophiles, lipids (e.g., cholesterol, a bile acid, or a fatty acid (e.g., lithocholic-oleyl, lauroyl, docosanyl, stearoyl, palmitoyl, myristoyl, oleoyl, linoleoyl), steroids (e.g., uvaol, hecigenin, diosgenin), terpenes (e.g., triterpenes, e.g., sarsasapogenin, Friedelin, epifriedelanol derivatized lithocholic acid), vitamins (e.g., folic acid, vitamin A, biotin, pyridoxal), carbohydrates, proteins, protein binding agents, integrin targeting molecules, polycationics, peptides,

polyamines, and peptide mimics. The ligand may also be a recombinant or synthetic molecule, such as a synthetic polymer, e.g., polyethylene glycol (PEG), PEG-40K, PEG-20K and PEG-5K. Other examples of ligands include lipophilic molecules, e.g., cholesterol, cholic acid, adamantane acetic acid, 1-pyrene butyric acid, dihydrotestosterone, glycerol (e.g., esters and ethers thereof, e.g., C₁₀, C₁₁, C₁₂, C₁₃, C₁₄, C₁₅, C₁₆, C₁₇, C₁₈, C₁₉, or C₂₀ alkyl; e.g., lauroyl, docosanyl, 5 stearyl, oleoyl, linoleoyl 1,3-bis-O(hexadecyl)glycerol, 1,3-bis-O(octadecyl)glycerol), geranyloxyhexyl group, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, O3-(oleoyl)lithocholic acid, O3-(oleoyl)cholenic acid, dodecanoyl, lithocholyl, 5 β -cholanyl, N,N-distearyl-lithocholamide, 1,2-di-O-stearoylglyceride, dimethoxytrityl, or phenoxazine) and PEG (e.g., PEG-5K, PEG-20K, PEG-40K). Preferred lipophilic moieties include lipid, cholesterol, oleyl, retinyl, or cholesteryl residues.

[0042] Conjugating a ligand to a dsRNA can enhance its cellular absorption, lipophilic compounds that have been conjugated to oligonucleotides include 1-pyrene butyric acid, 1,3-bis-O-(hexadecyl)glycerol, and menthol. One example of a ligand for receptor-mediated endocytosis is folic acid. Folic acid enters the cell by folate-receptor-mediated endocytosis. dsRNA compounds bearing folic acid would be efficiently transported into the cell via the folate-receptor-mediated endocytosis. Other ligands that have been conjugated to oligonucleotides include polyethylene glycols, carbohydrate clusters, cross-linking agents, porphyrin conjugates, delivery peptides and lipids such as cholesterol. In certain instances, conjugation of a cationic ligand to oligonucleotides results in improved resistance to nucleases. Representative examples of cationic ligands are propylammonium and dimethylpropylammonium. Interestingly, antisense oligonucleotides were reported to retain their high binding affinity to mRNA when the cationic ligand was dispersed, throughout the oligonucleotide. See M. Manoharan Antisense & Nucleic Acid Drug Development 2002, 12, 103 and references therein.

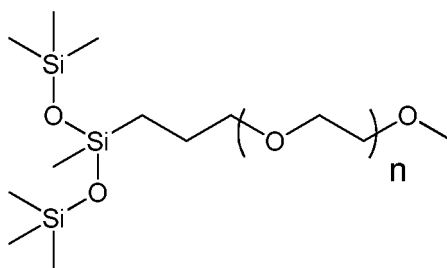
[0043] A biologic delivery can be accomplished by a variety of methods including, without limitation, (1) loading liposomes with a dsRNA acid molecule provided herein and (2) complexing a dsRNA molecule with lipids or liposomes to form nucleic acid-lipid or nucleic acid-liposome complexes. The liposome can be composed of cationic and neutral lipids commonly used to transfect cells in vitro. Cationic lipids can complex (e.g., charge-associate) with negatively charged, nucleic acids to form liposomes. Examples of cationic liposomes include, without limitation, lipofectin, lipofectamine, lipofectace, and DOTAP. Procedures for forming liposomes are well known in the art. Liposome compositions can be formed, for example, from phosphatidylcholine, dimyristoyl phosphatidylcholine, dipalmitoyl phosphatidylcholine, dimyristoyl phosphatidyl glycerol, dioleoyl phosphatidylethanolamine or liposomes comprising dihydrosphingomyelin (DHSM). Numerous lipophilic agents are commercially available, including Lipofectin® (Invitrogen/Life Technologies, Carlsbad, Calif.) and Effectene™ (Qiagen, Valencia, Calif.). In addition, systemic delivery methods can be optimized using commercially available cationic lipids such as DDAB or DOTAP, each of which can be mixed with a neutral lipid such as DOPE or cholesterol. In some cases, liposomes such as those described by Templeton et al. (Nature Biotechnology, 15:647-652 (1997)) can be used. In other embodiments, polycations such as polyethyleneimine can be used to achieve delivery in vivo and ex vivo (Boletta et al., J. Am Soc. Nephrol. 7:1728 (1996)). Additional information regarding the use of liposomes to deliver nucleic acids can be found in U.S. Pat. No. 6,271,359, PCT Publication WO 96/40964 and Morrissey, D. et al. 2005. Nat Biotechnol. 23(8):1002-7.

[0044] In certain embodiments, an organosilicone preparation that is commercially available as Silwet® L-77 surfactant having CAS Number 27306-78-1 and EPA Number: CAL.REG.NO. 5905-50073-AA, and currently available from Momentive Performance Materials, Albany, New York can be used to prepare a polynucleotide composition. In certain embodiments where a Silwet L-77 organosilicone preparation is used as a pre-spray treatment of plant leaves or other plant surfaces, freshly made concentrations in the range of about 0.1 to about 2 percent by weight (wt percent) (e.g., about 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.5 wt percent) are efficacious in preparing a leaf or other plant surface for transfer of polynucleotide molecules into plant cells from a topical application on the surface. In certain embodiments of the methods and compositions provided herein, a composition that comprises a polynucleotide molecule and an organosilicone preparation comprising Silwet L-77 in the range of about 0.1 to about 2 percent by weight (wt percent) (e.g., 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.5 wt percent) is used or provided.

[0045] In certain embodiments, any of the commercially available organosilicone preparations provided such as the following Breakthru S 321, Breakthru S 200 Cat# 67674-67-3, Breakthru OE 441 Cat#68937-55-3, Breakthru S 278 Cat #27306-78-1, Breakthru S 243, Breakthru S 233 Cat#134180-76-0, available from manufacturer Evonik Goldschmidt (Germany), Silwet® HS 429, Silwet® HS 312, Silwet® HS 508, Silwet® HS 604 (Momentum Performance Materials, Albany, New York) can be used as transfer agents in a polynucleotide composition. In certain embodiments where an organosilicone preparation is used as a pre-spray treatment of plant leaves or other surfaces, freshly made concentrations in the range of about 0.1 to about 2 percent by weight (wt percent) (e.g., 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.5 wt percent) are efficacious in preparing a leaf or other plant surface for transfer of polynucleotide molecules into plant cells from a topical application on the surface. In certain embodiments of the methods and compositions provided herein, a composition that comprises a polynucleotide molecule and an organosilicone preparation in the range of about 0.1 to about 2 percent by weight (wt percent) (e.g., 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.5 wt percent) is used or

provided.

[0046] Organosilicone preparations used in the methods and compositions provided herein can comprise one or more effective organosilicone compounds. As used herein, the phrase "effective organosilicone compound" is used to describe any organosilicone compound that is found in an organosilicone preparation that enables a polynucleotide to enter a plant cell. In certain embodiments, an effective organosilicone compound can enable a polynucleotide to enter a plant cell in a manner permitting a polynucleotide mediated suppression of a target gene expression in the plant cell. In general, effective organosilicone compounds include, but are not limited to, compounds that can comprise: i) a trisiloxane head group that is covalently linked to, ii) an alkyl linker including, but not limited to, an n-propyl linker, that is covalently linked to, iii) a poly glycol chain, that is covalently linked to, iv) a terminal group. Trisiloxane head groups of such effective organosilicone compounds include, but are not limited to, heptamethyltrisiloxane. Alkyl linkers can include, but are not limited to, an n-propyl linker. Poly glycol chains include, but are not limited to, polyethylene glycol or polypropylene glycol. Poly glycol chains can comprise a mixture that provides an average chain length "n" of about "7.5". In certain embodiments, the average chain length "n" can vary from about 5 to about 14. Terminal groups can include, but are not limited to, alkyl groups such as a methyl group. Effective organosilicone compounds are believed to include, but are not limited to, trisiloxane ethoxylate surfactants or polyalkylene oxide modified heptamethyl trisiloxane.



(Compound I: polyalkyleneoxide heptamethyltrisiloxane, average $n=7.5$).

[0047] In certain embodiments, an organosilicone preparation that comprises an organosilicone compound comprising a trisiloxane head group is used in the methods and compositions provided herein. In certain embodiments, an organosilicone preparation that comprises an organosilicone compound comprising a heptamethyltrisiloxane head group is used in the methods and compositions provided herein. In certain embodiments, an organosilicone composition that comprises Compound I is used in the methods and compositions provided herein. In certain embodiments, an organosilicone composition that comprises Compound I is used in the methods and compositions provided herein. In certain embodiments of the methods and compositions provided herein, a composition that comprises a polynucleotide molecule and one or more effective organosilicone compound in the range of about 0.1 to about 2 percent by weight (wt percent) (e. g., 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.5 wt percent) is used or provided.

[0048] Compositions include but are not limited components that are one or more polynucleotides essentially identical to, or essentially complementary to a chloroplast import protein or import processing enzyme gene sequence (promoter, intron, exon, 5' untranslated region, 3' untranslated region), a transfer agent that provides for the polynucleotide to enter a plant cell, a herbicide that complements the action of the polynucleotide, one or more additional herbicides that further enhance the herbicide activity of the composition or provide an additional mode of action different from the complementing herbicide, various salts and stabilizing agents that enhance the utility of the composition as an admixture of the components of the composition.

[0049] In certain aspects, methods include one or more applications of a polynucleotide composition and one or more applications of a transfer agent for conditioning of a plant to permeation by polynucleotides. When the agent for conditioning to permeation is an organosilicone composition or compound contained therein, embodiments of the polynucleotide molecules are double-stranded RNA oligonucleotides, single-stranded RNA oligonucleotides, double-stranded RNA polynucleotides, single-stranded RNA polynucleotides, double-stranded DNA oligonucleotides, single-stranded DNA oligonucleotides, double-stranded DNA polynucleotides, single-stranded DNA polynucleotides, chemically modified RNA or DNA oligonucleotides or polynucleotides or mixtures thereof.

[0050] Compositions and methods are useful for modulating the expression a protein of an endogenous gene, wherein the protein is imported into a chloroplast and is a target of a herbicide, for example, an EPSPS gene or a transgenic EPSPS gene (for example, CP4 EPSPS, U.S. Pat. No. RE39,247 and 2mEPSPS, U.S. Pat. No. 6,040,497) gene in a plant cell. In various embodiments, an EPSPS gene includes coding (protein-coding or translatable) sequence, non-coding (non-translatable) sequence, or both coding and non-coding sequence. Compositions can include polynucleotides and oligonucleotides designed to target one or more chloroplast import genes and a herbicide target gene, or multiple

segments of one or more the genes. The gene can include multiple consecutive segments, multiple nonconsecutive segments of a target gene, multiple alleles of a target gene, or multiple target genes from one or more species.

[0051] Provided is a method for modulating expression of a chloroplast import gene or chloroplast protein processing gene in a plant including (a) conditioning of a plant to permeation by polynucleotides and (b) treatment of the plant with the polynucleotide molecules, wherein the polynucleotide molecules include at least one segment of 19 or more, 25 or more, 30 or more, 40 or more, 45 or more, or 50 or more contiguous nucleotides cloned from or otherwise identified from the target gene in either anti-sense or sense orientation, whereby the polynucleotide molecules permeate the interior of the plant and induce modulation of the target gene. The conditioning and polynucleotide application can be performed separately or in a single step. When the conditioning and polynucleotide application are performed in separate steps, the conditioning can precede or can follow the polynucleotide application within minutes, hours, or days. In some embodiments more than one conditioning step or more than one polynucleotide molecule application can be performed on the same plant. In embodiments of the method, the segment can be cloned or identified from (a) coding (protein-encoding), (b) non-coding (promoter and other gene related molecules), or (c) both coding and non-coding parts of the target gene. Non-coding parts include DNA, such as promoter regions or the RNA transcribed by the DNA that provide RNA regulatory molecules, including but not limited to: introns, 5' or 3' untranslated regions, and microRNAs (miRNA), *trans*-acting siRNAs, natural anti-sense siRNAs, and other small RNAs with regulatory function or RNAs having structural or enzymatic function including but not limited to: ribozymes, ribosomal RNAs, t-RNAs, aptamers, and riboswitches.

[0052] The following examples are included to demonstrate examples of certain preferred embodiments.

EXAMPLES

Example 1. Polynucleotides related to the plant chloroplast protein import system and target gene sequences thereof.

[0053] The target chloroplast protein import system naturally occurs in the genome of plants, including but not limited to *Abutilon theophrasti*, *Alopecurus myosuroides*, *Amaranthus albus*, *Amaranthus chlorostachys*, *Amaranthus graecizans*, *Amaranthus hybridus*, *Amaranthus lividus*, *Amaranthus palmeri*, *Amaranthus rudis*, *Amaranthus spinosus*, *Amaranthus thunbergii*, *Amaranthus viridis*, *Ambrosia artemisiifolia*, *Ambrosia trifida*, *Avena fatua*, *Chenopodium album*, *Commelina diffusa*, *Convolvulus arvensis*, *Conyza canadensis*, *Cyperus esculentus*, *Digitaria sanguinalis*, *Echinochloa colona*, *Echinochloa crus-galli*, *Euphorbia heterophylla*, *Festuca arundinacea*, *Ipomoea hederacea*, *Kochia scoparia*, *Lolium arundinaceum*, *Lolium multiflorum*, *Lolium rigidum*, *Portulaca oleracea*, *Senna obtusifolia*, *Setaria viridis*, *Sorghum halepense*, *Spirodela polyrrhiza*, *Taraxacum officinale*, *Trifolium repens*, *Xanthium strumarium* and other weed species that include molecules related to the expression of a polypeptide identified as an enzyme or protein of a chloroplast import protein system, that include regulatory molecules, cDNAs comprising coding and noncoding regions of the gene and fragments thereof as shown in SEQ ID NO: 1-1263 and SEQ ID NO: 1584-1683, summarized in Table 1.

[0054] Polynucleotide molecules are extracted from these plant species by methods standard in the field, for example, total RNA is extracted using Trizol Reagent (Invitrogen Corp, Carlsbad, CA Cat. No. 15596-018), following the manufacturer's protocol or modifications thereof by those skilled in the art of polynucleotide extraction that may enhance recover or purity of the extracted RNA. Briefly, start with 1 gram of ground plant tissue for extraction. Prealiquot 10 milliliters (mL) Trizol reagent to 15 mL conical tubes. Add ground powder to tubes and shake to homogenize. Incubate the homogenized samples for 5 minutes (min) at room temperature (RT) and then add 3 mL of chloroform. Shake tubes vigorously by hand for 15-30 seconds (sec) and incubate at RT for 3 min. Centrifuge the tubes at 7,000 revolutions per minute (rpm) for 10 min at 4 degrees C (centigrade). Transfer the aqueous phase to a new 1.5 mL tube and add 1 volume of cold isopropanol. Incubate the samples for 20-30 min at RT and centrifuge at 10,000 rpm for 10 min at 4 degrees C. Wash pellet with Sigma-grade 80 percent ethanol. Remove the supernatant and briefly air-dry the pellet. Dissolve the RNA pellet in approximately 200 microliters of DEPC treated water. Heat briefly at 65 degrees C to dissolve pellet and vortex or pipet to resuspend RNA pellet. Adjust RNA to 1-2 microgram/microliter.

[0055] DNA is extracted using EZNA SP Plant DNA Mini kit (Omega Biotek, Norcross GA, Cat#D5511) and Lysing Matrix E tubes (Q-Biogen, Cat#6914), following the manufacturer's protocol or modifications thereof by those skilled in the art of polynucleotide extraction that may enhance recover or purity of the extracted DNA. Briefly, aliquot ground tissue to a Lysing Matrix E tube on dry ice, add 800 μ L Buffer SP1 to each sample, homogenize in a bead beater for 35-45sec, incubate on ice for 45-60 sec, centrifuge at ≥ 14000 rpm for 1min at RT, add 10 microliter RNase A to the lysate, incubate at 65°C for 10min, centrifuge for 1min at RT, add 280 μ L Buffer SP2 and vortex to mix, incubate the samples on ice for 5min, centrifuge at $\geq 10,000g$ for 10min at RT, transfer the supernatant to a homogenizer column in a 2ml collection tube, centrifuge at 10,000g for 2min at RT, transfer the cleared lysate into a 1.5ml microfuge tube, add 1.5 volumes Buffer SP3 to the cleared lysate, vortex immediately to obtain a homogeneous mixture, transfer up to 650 μ L supernatant to the Hi-Bind column, centrifuge at 10,000g for 1min, repeat, apply 100 μ L 65°C Elution Buffer to the column, centrifuge at 10,000g for 5min at RT.

[0056] Next-generation DNA sequencers, such as the 454-FLX (Roche, Branford, CT), the SOLiD (Applied Biosys-

tems), and the Genome Analyzer (HiSeq2000, Illumina, San Diego, CA) are used to provide polynucleotide sequence from the DNA and RNA extracted from the plant tissues. Raw sequence data is assembled into contigs. The contig sequence is used to identify trigger polynucleotide molecules that can be applied to the plant to enable regulation of the gene expression and result in an agronomic benefit.

Table 1. Target chloroplast import protein system DNA sequence contigs from the various plant species .

SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
1	TOC159	Abutilon theophrasti	cDNA
2	TOC159	Abutilon theophrasti	cDNA
3	TOC159	Abutilon theophrasti	gDNA
4	TOC159	Abutilon theophrasti	gDNA
5	TOC159	Abutilon theophrasti	gDNA
6	TOC159	Abutilon theophrasti	gDNA
7	TOC159	Abutilon theophrasti	gDNA
8	TOC159	Abutilon theophrasti	gDNA
9	TOC159	Abutilon theophrasti	gDNA
10	TOC159	Abutilon theophrasti	gDNA
11	TOC159	Abutilon theophrasti	gDNA
12	TOC159	Abutilon theophrasti	gDNA
13	TOC159	Abutilon theophrasti	gDNA
14	TOC159	<i>Alopecurus myosuroides</i>	cDNA
15	TOC159	Amaranthus albus	cDNA
16	TOC159	Amaranthus albus	cDNA
17	TOC159	Amaranthus albus	cDNA
18	TOC159	Amaranthus chlorostachys	cDNA
19	TOC159	Amaranthus graecizans	cDNA
20	TOC159	Amaranthus graecizans	cDNA
21	TOC159	Amaranthus hybridus	cDNA
22	TOC159	Amaranthus hybridus	cDNA
23	TOC159	Amaranthus lividus	cDNA
24	TOC159	Amaranthus palmeri	cDNA
25	TOC159	Amaranthus palmeri	cDNA
26	TOC159	Amaranthus palmeri	cDNA
27	TOC159	Amaranthus palmeri	gDNA
28	TOC159	Amaranthus palmeri	gDNA
29	TOC159	Amaranthus rudis	cDNA
30	TOC159	Amaranthus rudis	gDNA
31	TOC159	Amaranthus rudis	gDNA
32	TOC159	Amaranthus rudis	gDNA
33	TOC159	Amaranthus spinosus	cDNA
34	TOC159	Amaranthus spinosus	cDNA
35	TOC159	Amaranthus thunbergii	cDNA

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(continued)

SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
36	TOC159	Amaranthus thunbergii	cDNA
37	TOC159	Amaranthus thunbergii	cDNA
38	TOC159	Amaranthus thunbergii	cDNA
39	TOC159	Amaranthus viridis	cDNA
40	TOC159	Amaranthus viridis	cDNA
41	TOC159	Ambrosia artemisiifolia	gDNA
42	TOC159	Ambrosia artemisiifolia	gDNA
43	TOC159	Ambrosia trifida	cDNA
44	TOC159	Ambrosia trifida	cDNA
45	TOC159	Ambrosia trifida	gDNA
46	TOC159	Ambrosia trifida	gDNA
47	TOC159	Ambrosia trifida	gDNA
48	TOC159	Ambrosia trifida	gDNA
49	TOC159	Ambrosia trifida	gDNA
50	TOC159	Ambrosia trifida	gDNA
51	TOC159	Ambrosia trifida	gDNA
52	TOC159	Ambrosia trifida	gDNA
53	TOC159	Ambrosia trifida	gDNA
54	TOC159	Ambrosia trifida	gDNA
55	TOC159	Ambrosia trifida	gDNA
56	TOC159	Ambrosia trifida	gDNA
57	TOC159	Ambrosia trifida	gDNA
58	TOC159	Ambrosia trifida	gDNA
59	TOC159	Ambrosia trifida	gDNA
60	TOC159	Avena fatua	cDNA
61	TOC159	Avena fatua	cDNA
62	TOC159	Chenopodium album	cDNA
63	TOC159	Chenopodium album	cDNA
64	TOC159	Chenopodium album	cDNA
65	TOC159	Convolvulus arvensis	cDNA
66	TOC159	Convolvulus arvensis	cDNA
67	TOC159	Conyza canadensis	cDNA
68	TOC159	Conyza canadensis	gDNA
69	TOC159	Cyperus esculentus	gDNA
70	TOC159	Digitaria sanguinalis	cDNA
71	TOC159	Digitaria sanguinalis	cDNA
72	TOC159	Digitaria sanguinalis	cDNA
73	TOC159	Digitaria sanguinalis	cDNA

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(continued)

SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
74	TOC159	Digitaria sanguinalis	cDNA
75	TOC159	Digitaria sanguinalis	gDNA
76	TOC159	Digitaria sanguinalis	gDNA
77	TOC159	Echinochloa colona	cDNA
78	TOC159	Echinochloa colona	cDNA
79	TOC159	Echinochloa crus-galli	cDNA
80	TOC159	Euphorbia heterophylla	cDNA
81	TOC159	Euphorbia heterophylla	cDNA
82	TOC159	Euphorbia heterophylla	cDNA
83	TOC159	Euphorbia heterophylla	gDNA
84	TOC159	Festuca arundinacea	gDNA
85	TOC159	Festuca arundinacea	gDNA
86	TOC159	Festuca arundinacea	gDNA
87	TOC159	Ipomoea hederacea	cDNA
88	TOC159	Kochia scoparia	gDNA
89	TOC159	Lolium arundinaceum	gDNA
90	TOC159	Lolium arundinaceum	gDNA
91	TOC159	Lolium multiflorum	cDNA
92	TOC159	Lolium multiflorum	cDNA
93	TOC159	Lolium multiflorum	gDNA
94	TOC159	Lolium multiflorum	gDNA
95	TOC159	Lolium multiflorum	gDNA
96	TOC159	Lolium multiflorum	gDNA
97	TOC159	Lolium multiflorum	gDNA
98	TOC159	Lolium multiflorum	gDNA
99	TOC159	Lolium rigidum	gDNA
100	TOC159	Lolium rigidum	gDNA
101	TOC159	Portulaca oleracea	gDNA
102	TOC159	Portulaca oleracea	gDNA
103	TOC159	Portulaca oleracea	gDNA
104	TOC159	Senna obtusifolia	cDNA
105	TOC159	Senna obtusifolia	cDNA
106	TOC159	Sorghum halepense	cDNA
107	TOC159	Sorghum halepense	cDNA
108	TOC159	Sorghum halepense	gDNA
109	TOC159	Spirodela polyrrhiza	gDNA
110	TOC159	Taraxacum officinale	gDNA
111	TOC159	Trifolium repens	gDNA

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(continued)

SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
112	TOC159	Trifolium repens	gDNA
113	TOC159	Trifolium repens	gDNA
114	TOC159	Trifolium repens	gDNA
115	TOC159	Trifolium repens	gDNA
116	TOC159	Xanthium strumarium	cDNA
117	TOC159	Xanthium strumarium	cDNA
118	TOC33	Amaranthus palmeri	cDNA
119	TOC33	Amaranthus palmeri	gDNA
120	TOC33	Amaranthus palmeri	gDNA
121	TOC33	Amaranthus palmeri	gDNA
122	TOC33	Amaranthus rudis	cDNA
123	TOC33	Amaranthus rudis	gDNA
124	TOC33	Amaranthus rudis	gDNA
125	TOC33	Amaranthus rudis	gDNA
126	TOC33	Ambrosia artemisiifolia	gDNA
127	TOC33	Ambrosia artemisiifolia	gDNA
128	TOC33	Ambrosia artemisiifolia	gDNA
129	TOC33	Ambrosia artemisiifolia	gDNA
130	TOC33	Ambrosia trifida	cDNA
131	TOC33	Ambrosia trifida	gDNA
132	TOC33	Ambrosia trifida	gDNA
133	TOC33	Commelina diffusa	cDNA
134	TOC33	Cyperus esculentus	gDNA
135	TOC33	Cyperus esculentus	gDNA
136	TOC33	Euphorbia heterophylla	cDNA
137	TOC33	Euphorbia heterophylla	gDNA
138	TOC33	Festuca arundinacea	gDNA
139	TOC33	Festuca arundinacea	gDNA
140	TOC33	Festuca arundinacea	gDNA
141	TOC33	Lolium arundinaceum	gDNA
142	TOC33	Portulaca oleracea	gDNA
143	TOC33	Portulaca oleracea	gDNA
144	TOC33	Senna obtusifolia	cDNA
145	TOC33	Sorghum halepense	gDNA
146	TOC33	Sorghum halepense	gDNA
147	TOC33	Sorghum halepense	gDNA
148	TOC33	Spirodela polyrrhiza	gDNA
149	TOC33	Taraxacum officinale	gDNA

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(continued)

SEQ ID NO	GENE	SPECIES	SEQ_TY P E
150	TOC33	Taraxacum officinale	gDNA
151	TOC33	Trifolium repens	gDNA
152	TOC33	Trifolium repens	gDNA
153	TOC33	Trifolium repens	gDNA
154	TOC33	Trifolium repens	gDNA
155	TOC33	Xanthium strumarium	cDNA
156	TOC34	Abutilon theophrasti	cDNA
157	TOC34	Abutilon theophrasti	gDNA
158	TOC34	Abutilon theophrasti	gDNA
159	TOC34	Abutilon theophrasti	gDNA
160	TOC34	Abutilon theophrasti	gDNA
161	TOC34	Abutilon theophrasti	gDNA
162	TOC34	Alopecurus myosuroides	cDNA
163	TOC34	Alopecurus myosuroides	cDNA
164	TOC34	Amaranthus albus	cDNA
165	TOC34	Amaranthus graecizans	cDNA
166	TOC34	Amaranthus hybridus	cDNA
167	TOC34	Amaranthus lividus	cDNA
168	TOC34	Amaranthus palmeri	cDNA
169	TOC34	Amaranthus palmeri	gDNA
170	TOC34	Amaranthus palmeri	gDNA
171	TOC34	Amaranthus rudis	cDNA
172	TOC34	Amaranthus rudis	gDNA
173	TOC34	Amaranthus rudis	gDNA
174	TOC34	Amaranthus rudis	gDNA
175	TOC34	Amaranthus rudis	gDNA
176	TOC34	Amaranthus rudis	gDNA
177	TOC34	Amaranthus rudis	gDNA
178	TOC34	Amaranthus spinosus	cDNA
179	TOC34	Amaranthus thunbergii	cDNA
180	TOC34	Amaranthus viridis	cDNA
181	TOC34	Ambrosia artemisiifolia	gDNA
182	TOC34	Ambrosia artemisiifolia	gDNA
183	TOC34	Ambrosia artemisiifolia	gDNA
184	TOC34	Ambrosia artemisiifolia	gDNA
185	TOC34	Ambrosia artemisiifolia	gDNA
186	TOC34	Ambrosia trifida	cDNA
187	TOC34	Ambrosia trifida	gDNA

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(continued)

SEQ ID NO	GENE	SPECIES	SEQ_TY P E
188	TOC34	Ambrosia trifida	gDNA
189	TOC34	Ambrosia trifida	gDNA
190	TOC34	Ambrosia trifida	gDNA
191	TOC34	Ambrosia trifida	gDNA
192	TOC34	Ambrosia trifida	gDNA
193	TOC34	Chenopodium album	cDNA
194	TOC34	Commelina diffusa	cDNA
195	TOC34	Commelina diffusa	cDNA
196	TOC34	Commelina diffusa	cDNA
197	TOC34	Conyza canadensis	cDNA
198	TOC34	Conyza canadensis	gDNA
199	TOC34	Cyperus esculentus	gDNA
200	TOC34	Cyperus esculentus	gDNA
201	TOC34	Cyperus esculentus	gDNA
202	TOC34	Digitaria sanguinalis	cDNA
203	TOC34	Echinochloa crus-galli	cDNA
204	TOC34	Euphorbia heterophylla	cDNA
205	TOC34	Euphorbia heterophylla	gDNA
206	TOC34	Festuca arundinacea	gDNA
207	TOC34	Festuca arundinacea	gDNA
208	TOC34	Festuca arundinacea	gDNA
209	TOC34	Festuca arundinacea	gDNA
210	TOC34	Festuca arundinacea	gDNA
211	TOC34	Festuca arundinacea	gDNA
212	TOC34	Ipomoea hederacea	cDNA
213	TOC34	Kochia scoparia	gDNA
214	TOC34	Kochia scoparia	gDNA
215	TOC34	Lolium arundinaceum	gDNA
216	TOC34	Lolium arundinaceum	gDNA
217	TOC34	Lolium arundinaceum	gDNA
218	TOC34	Lolium multiflorum	cDNA
219	TOC34	Lolium multiflorum	gDNA
220	TOC34	Lolium multiflorum	gDNA
221	TOC34	Lolium multiflorum	gDNA
222	TOC34	Lolium multiflorum	gDNA
223	TOC34	Lolium rigidum	gDNA
224	TOC34	Lolium rigidum	gDNA
225	TOC34	Lolium rigidum	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
226	TOC34	Lolium rigidum	gDNA
227	TOC34	Portulaca oleracea	gDNA
228	TOC34	Portulaca oleracea	gDNA
229	TOC34	Portulaca oleracea	gDNA
230	TOC34	Portulaca oleracea	gDNA
231	TOC34	Senna obtusifolia	cDNA
232	TOC34	Sorghum halepense	gDNA
233	TOC34	Sorghum halepense	gDNA
234	TOC34	Sorghum halepense	gDNA
235	TOC34	Spirodela polyrrhiza	gDNA
236	TOC34	Taraxacum officinale	gDNA
237	TOC34	Taraxacum officinale	gDNA
238	TOC34	Taraxacum officinale	gDNA
239	TOC34	Taraxacum officinale	gDNA
240	TOC34	Trifolium repens	gDNA
241	TOC34	Trifolium repens	gDNA
242	TOC34	Trifolium repens	gDNA
243	TOC34	Trifolium repens	gDNA
244	TOC34	Trifolium repens	gDNA
245	TOC34	Trifolium repens	gDNA
246	TOC34	Xanthium strumarium	cDNA
247	TOC34	Xanthium strumarium	cDNA
248	TOC75	Abutilon theophrasti	cDNA
249	TOC75	Abutilon theophrasti	gDNA
250	TOC75	Abutilon theophrasti	gDNA
251	TOC75	Abutilon theophrasti	gDNA
252	TOC75	Abutilon theophrasti	gDNA
253	TOC75	Abutilon theophrasti	gDNA
254	TOC75	Amaranthus albus	cDNA
255	TOC75	Amaranthus albus	cDNA
256	TOC75	Amaranthus chlorostachys	cDNA
257	TOC75	Amaranthus graecizans	cDNA
258	TOC75	Amaranthus hybridus	cDNA
259	TOC75	Amaranthus lividus	cDNA
260	TOC75	Amaranthus palmeri	cDNA
261	TOC75	Amaranthus palmeri	gDNA
262	TOC75	Amaranthus palmeri	gDNA
263	TOC75	Amaranthus palmeri	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
264	TOC75	Amaranthus rudis	cDNA
265	TOC75	Amaranthus rudis	gDNA
266	TOC75	Amaranthus rudis	gDNA
267	TOC75	Amaranthus rudis	gDNA
268	TOC75	Amaranthus rudis	gDNA
269	TOC75	Amaranthus rudis	gDNA
270	TOC75	Amaranthus rudis	gDNA
271	TOC75	Amaranthus rudis	gDNA
272	TOC75	Amaranthus spinosus	cDNA
273	TOC75	Amaranthus thunbergii	cDNA
274	TOC75	Amaranthus viridis	cDNA
275	TOC75	Ambrosia artemisiifolia	gDNA
276	TOC75	Ambrosia artemisiifolia	gDNA
277	TOC75	Ambrosia artemisiifolia	gDNA
278	TOC75	Ambrosia artemisiifolia	gDNA
279	TOC75	Ambrosia artemisiifolia	gDNA
280	TOC75	Ambrosia trifida	cDNA
281	TOC75	Ambrosia trifida	gDNA
282	TOC75	Ambrosia trifida	gDNA
283	TOC75	Ambrosia trifida	gDNA
284	TOC75	Ambrosia trifida	gDNA
285	TOC75	Ambrosia trifida	gDNA
286	TOC75	Ambrosia trifida	gDNA
287	TOC75	Ambrosia trifida	gDNA
288	TOC75	Ambrosia trifida	gDNA
289	TOC75	Ambrosia trifida	gDNA
290	TOC75	Ambrosia trifida	gDNA
291	TOC75	Chenopodium album	cDNA
292	TOC75	Commelina diffusa	cDNA
293	TOC75	Commelina diffusa	cDNA
294	TOC75	Convolvulus arvensis	cDNA
295	TOC75	Conyza canadensis	cDNA
296	TOC75	Conyza canadensis	cDNA
297	TOC75	Conyza canadensis	gDNA
298	TOC75	Cyperus esculentus	gDNA
299	TOC75	Digitaria sanguinalis	cDNA
300	TOC75	Digitaria sanguinalis	cDNA
301	TOC75	Digitaria sanguinalis	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
302	TOC75	Digitaria sanguinalis	gDNA
303	TOC75	Echinochloa crus-galli	cDNA
304	TOC75	Echinochloa crus-galli	cDNA
305	TOC75	Euphorbia heterophylla	cDNA
306	TOC75	Euphorbia heterophylla	gDNA
307	TOC75	Festuca arundinacea	gDNA
308	TOC75	Festuca arundinacea	gDNA
309	TOC75	Festuca arundinacea	gDNA
310	TOC75	Festuca arundinacea	gDNA
311	TOC75	Festuca arundinacea	gDNA
312	TOC75	Festuca arundinacea	gDNA
313	TOC75	Festuca arundinacea	gDNA
314	TOC75	Festuca arundinacea	gDNA
315	TOC75	Festuca arundinacea	gDNA
316	TOC75	Festuca arundinacea	gDNA
317	TOC75	Ipomoea hederacea	cDNA
318	TOC75	Kochia scoparia	gDNA
319	TOC75	Kochia scoparia	gDNA
320	TOC75	Kochia scoparia	gDNA
321	TOC75	Kochia scoparia	gDNA
322	TOC75	Kochia scoparia	gDNA
323	TOC75	Kochia scoparia	gDNA
324	TOC75	Lolium arundinaceum	gDNA
325	TOC75	Lolium arundinaceum	gDNA
326	TOC75	Lolium arundinaceum	gDNA
327	TOC75	Lolium arundinaceum	gDNA
328	TOC75	Lolium arundinaceum	gDNA
329	TOC75	Lolium rigidum	gDNA
330	TOC75	Lolium rigidum	gDNA
331	TOC75	Lolium rigidum	gDNA
332	TOC75	Lolium rigidum	gDNA
333	TOC75	Lolium rigidum	gDNA
334	TOC75	Portulaca oleracea	gDNA
335	TOC75	Portulaca oleracea	gDNA
336	TOC75	Portulaca oleracea	gDNA
337	TOC75	Senna obtusifolia	cDNA
338	TOC75	Sorghum halepense	gDNA
339	TOC75	Sorghum halepense	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
340	TOC75	Spirodela polyrrhiza	gDNA
341	TOC75	Taraxacum officinale	gDNA
342	TOC75	Trifolium repens	gDNA
343	TOC75	Trifolium repens	gDNA
344	TOC75	Trifolium repens	gDNA
345	TOC75	Trifolium repens	gDNA
346	TOC75	Trifolium repens	gDNA
347	TOC75	Trifolium repens	gDNA
348	TOC75	Xanthium strumarium	cDNA
349	OEP80	Abutilon theophrasti	cDNA
350	OEP80	Abutilon theophrasti	cDNA
351	OEP80	Abutilon theophrasti	gDNA
352	OEP80	Abutilon theophrasti	gDNA
353	OEP80	Abutilon theophrasti	gDNA
354	OEP80	Abutilon theophrasti	gDNA
355	OEP80	Abutilon theophrasti	gDNA
356	OEP80	Abutilon theophrasti	gDNA
357	OEP80	Abutilon theophrasti	gDNA
358	OEP80	Amaranthus graecizans	cDNA
359	OEP80	Amaranthus graecizans	cDNA
360	OEP80	Amaranthus hybridus	cDNA
361	OEP80	Amaranthus hybridus	cDNA
362	OEP80	Amaranthus lividus	cDNA
363	OEP80	Amaranthus lividus	cDNA
364	OEP80	Amaranthus lividus	cDNA
365	OEP80	Amaranthus palmeri	cDNA
366	OEP80	Amaranthus palmeri	gDNA
367	OEP80	Amaranthus rudis	cDNA
368	OEP80	Amaranthus rudis	cDNA
369	OEP80	Amaranthus rudis	cDNA
370	OEP80	Amaranthus rudis	gDNA
371	OEP80	Amaranthus rudis	gDNA
372	OEP80	Amaranthus rudis	gDNA
373	OEP80	Amaranthus rudis	gDNA
374	OEP80	Amaranthus rudis	gDNA
375	OEP80	Amaranthus rudis	gDNA
376	OEP80	Amaranthus spinosus	cDNA
377	OEP80	Amaranthus spinosus	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
378	OEP80	Amaranthus thunbergii	cDNA
379	OEP80	Amaranthus viridis	cDNA
380	OEP80	Amaranthus viridis	cDNA
381	OEP80	Ambrosia artemisiifolia	gDNA
382	OEP80	Ambrosia artemisiifolia	gDNA
383	OEP80	Ambrosia artemisiifolia	gDNA
384	OEP80	Ambrosia artemisiifolia	gDNA
385	OEP80	Ambrosia artemisiifolia	gDNA
386	OEP80	Ambrosia artemisiifolia	gDNA
387	OEP80	Ambrosia trifida	cDNA
388	OEP80	Ambrosia trifida	cDNA
389	OEP80	Ambrosia trifida	gDNA
390	OEP80	Ambrosia trifida	gDNA
391	OEP80	Ambrosia trifida	gDNA
392	OEP80	Ambrosia trifida	gDNA
393	OEP80	Ambrosia trifida	gDNA
394	OEP80	Ambrosia trifida	gDNA
395	OEP80	Chenopodium album	cDNA
396	OEP80	Conyza canadensis	cDNA
397	OEP80	Conyza canadensis	cDNA
398	OEP80	Conyza canadensis	gDNA
399	OEP80	Conyza canadensis	gDNA
400	OEP80	Cyperus esculentus	gDNA
401	OEP80	Cyperus esculentus	gDNA
402	OEP80	Cyperus esculentus	gDNA
403	OEP80	Echinochloa colona	cDNA
404	OEP80	Echinochloa crus-galli	cDNA
405	OEP80	Echinochloa crus-galli	cDNA
406	OEP80	Euphorbia heterophylla	cDNA
407	OEP80	Euphorbia heterophylla	cDNA
408	OEP80	Euphorbia heterophylla	cDNA
409	OEP80	Euphorbia heterophylla	gDNA
410	OEP80	Euphorbia heterophylla	gDNA
411	OEP80	Euphorbia heterophylla	gDNA
412	OEP80	Euphorbia heterophylla	gDNA
413	OEP80	Euphorbia heterophylla	gDNA
414	OEP80	Festuca arundinacea	gDNA
415	OEP80	Festuca arundinacea	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
416	OEP80	Festuca arundinacea	gDNA
417	OEP80	Festuca arundinacea	gDNA
418	OEP80	Festuca arundinacea	gDNA
419	OEP80	Festuca arundinacea	gDNA
420	OEP80	Festuca arundinacea	gDNA
421	OEP80	Festuca arundinacea	gDNA
422	OEP80	Festuca arundinacea	gDNA
423	OEP80	Festuca arundinacea	gDNA
424	OEP80	Festuca arundinacea	gDNA
425	OEP80	Ipomoea hederacea	cDNA
426	OEP80	Ipomoea hederacea	cDNA
427	OEP80	Kochia scoparia	gDNA
428	OEP80	Lolium arundinaceum	gDNA
429	OEP80	Lolium arundinaceum	gDNA
430	OEP80	Lolium arundinaceum	gDNA
431	OEP80	Lolium arundinaceum	gDNA
432	OEP80	Lolium arundinaceum	gDNA
433	OEP80	Lolium arundinaceum	gDNA
434	OEP80	Lolium arundinaceum	gDNA
435	OEP80	Lolium arundinaceum	gDNA
436	OEP80	Lolium arundinaceum	gDNA
437	OEP80	Lolium arundinaceum	gDNA
438	OEP80	Lolium arundinaceum	gDNA
439	OEP80	Lolium arundinaceum	gDNA
440	OEP80	Lolium multiflorum	cDNA
441	OEP80	Lolium multiflorum	gDNA
442	OEP80	Lolium multiflorum	gDNA
443	OEP80	Lolium multiflorum	gDNA
444	OEP80	Lolium multiflorum	gDNA
445	OEP80	Lolium multiflorum	gDNA
446	OEP80	Lolium rigidum	gDNA
447	OEP80	Lolium rigidum	gDNA
448	OEP80	Lolium rigidum	gDNA
449	OEP80	Lolium rigidum	gDNA
450	OEP80	Lolium rigidum	gDNA
451	OEP80	Lolium rigidum	gDNA
452	OEP80	Lolium rigidum	gDNA
453	OEP80	Lolium rigidum	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TYP E
454	OEP80	Lolium rigidum	gDNA
455	OEP80	Portulaca oleracea	gDNA
456	OEP80	Portulaca oleracea	gDNA
457	OEP80	Portulaca oleracea	gDNA
458	OEP80	Portulaca oleracea	gDNA
459	OEP80	Portulaca oleracea	gDNA
460	OEP80	Portulaca oleracea	gDNA
461	OEP80	Senna obtusifolia	cDNA
462	OEP80	Senna obtusifolia	cDNA
463	OEP80	Sorghum halepense	gDNA
464	OEP80	Sorghum halepense	gDNA
465	OEP80	Sorghum halepense	gDNA
466	OEP80	Sorghum halepense	gDNA
467	OEP80	Sorghum halepense	gDNA
468	OEP80	Spirodela polyrrhiza	gDNA
469	OEP80	Spirodela polyrrhiza	gDNA
470	OEP80	Taraxacum officinale	gDNA
471	OEP80	Taraxacum officinale	gDNA
472	OEP80	Taraxacum officinale	gDNA
473	OEP80	Taraxacum officinale	gDNA
474	OEP80	Taraxacum officinale	gDNA
475	OEP80	Taraxacum officinale	gDNA
476	OEP80	Trifolium repens	gDNA
477	OEP80	Trifolium repens	gDNA
478	OEP80	Trifolium repens	gDNA
479	OEP80	Trifolium repens	gDNA
480	OEP80	Trifolium repens	gDNA
481	OEP80	Trifolium repens	gDNA
482	OEP80	Trifolium repens	gDNA
483	OEP80	Trifolium repens	gDNA
484	OEP80	Trifolium repens	gDNA
485	OEP80	Xanthium strumarium	cDNA
486	TOC132	Abutilon theophrasti	cDNA
487	TOC132	Abutilon theophrasti	cDNA
488	TOC132	Abutilon theophrasti	gDNA
489	TOC132	Abutilon theophrasti	gDNA
490	TOC132	Alopecurus myosuroides	cDNA
491	TOC132	Amaranthus albus	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
492	TOC132	Amaranthus graecizans	cDNA
493	TOC132	Amaranthus graecizans	cDNA
494	TOC132	Amaranthus hybridus	cDNA
495	TOC132	Amaranthus hybridus	cDNA
496	TOC132	Amaranthus hybridus	cDNA
497	TOC132	Amaranthus lividus	cDNA
498	TOC132	Amaranthus lividus	cDNA
499	TOC132	Amaranthus lividus	cDNA
500	TOC132	Amaranthus palmeri	cDNA
501	TOC132	Amaranthus palmeri	gDNA
502	TOC132	Amaranthus rudis	cDNA
503	TOC132	Amaranthus rudis	cDNA
504	TOC132	Amaranthus rudis	cDNA
505	TOC132	Amaranthus rudis	cDNA
506	TOC132	Amaranthus rudis	gDNA
507	TOC132	Amaranthus rudis	gDNA
508	TOC132	Amaranthus rudis	gDNA
509	TOC132	Amaranthus rudis	gDNA
510	TOC132	Amaranthus rudis	gDNA
511	TOC132	Amaranthus rudis	gDNA
512	TOC132	Amaranthus spinosus	cDNA
513	TOC132	Amaranthus spinosus	cDNA
514	TOC132	Amaranthus spinosus	cDNA
515	TOC132	Amaranthus thunbergii	cDNA
516	TOC132	Amaranthus thunbergii	cDNA
517	TOC132	Amaranthus viridis	cDNA
518	TOC132	Amaranthus viridis	cDNA
519	TOC132	Ambrosia artemisiifolia	gDNA
520	TOC132	Ambrosia trifida	cDNA
521	TOC132	Ambrosia trifida	cDNA
522	TOC132	Avena fatua	cDNA
523	TOC132	Chenopodium album	cDNA
524	TOC132	Chenopodium album	cDNA
525	TOC132	Commelina diffusa	cDNA
526	TOC132	Convolvulus arvensis	cDNA
527	TOC132	Convolvulus arvensis	cDNA
528	TOC132	Conyza canadensis	cDNA
529	TOC132	Conyza canadensis	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
530	TOC132	Conyza canadensis	cDNA
531	TOC132	Conyza canadensis	gDNA
532	TOC132	Conyza canadensis	gDNA
533	TOC132	Cyperus esculentus	gDNA
534	TOC132	Digitaria sanguinalis	cDNA
535	TOC132	Digitaria sanguinalis	cDNA
536	TOC132	Echinochloa colona	cDNA
537	TOC132	Echinochloa crus-galli	cDNA
538	TOC132	Euphorbia heterophylla	cDNA
539	TOC132	Euphorbia heterophylla	cDNA
540	TOC132	Euphorbia heterophylla	cDNA
541	TOC132	Euphorbia heterophylla	cDNA
542	TOC132	Euphorbia heterophylla	gDNA
543	TOC132	Euphorbia heterophylla	gDNA
544	TOC132	Euphorbia heterophylla	gDNA
545	TOC132	Festuca arundinacea	gDNA
546	TOC132	Festuca arundinacea	gDNA
547	TOC132	Festuca arundinacea	gDNA
548	TOC132	Festuca arundinacea	gDNA
549	TOC132	Festuca arundinacea	gDNA
550	TOC132	Festuca arundinacea	gDNA
551	TOC132	Ipomoea hederacea	cDNA
552	TOC132	Kochia scoparia	gDNA
553	TOC132	Kochia scoparia	gDNA
554	TOC132	Lolium arundinaceum	gDNA
555	TOC132	Lolium arundinaceum	gDNA
556	TOC132	Lolium rigidum	gDNA
557	TOC132	Portulaca oleracea	gDNA
558	TOC132	Portulaca oleracea	gDNA
559	TOC132	Portulaca oleracea	gDNA
560	TOC132	Senna obtusifolia	cDNA
561	TOC132	Senna obtusifolia	cDNA
562	TOC132	Sorghum halepense	gDNA
563	TOC132	Spirodela polyrrhiza	gDNA
564	TOC132	Taraxacum officinale	gDNA
565	TOC132	Taraxacum officinale	gDNA
566	TOC132	Trifolium repens	gDNA
567	TOC132	Trifolium repens	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
568	TOC132	Xanthium strumarium	cDNA
569	TOC132	Xanthium strumarium	cDNA
570	TIC110	Abutilon theophrasti	cDNA
571	TIC110	Abutilon theophrasti	gDNA
572	TIC110	Abutilon theophrasti	gDNA
573	TIC110	Abutilon theophrasti	gDNA
574	TIC110	Abutilon theophrasti	gDNA
575	TIC110	Abutilon theophrasti	gDNA
576	TIC110	Abutilon theophrasti	gDNA
577	TIC110	Abutilon theophrasti	gDNA
578	TIC110	Alopecurus myosuroides	cDNA
579	TIC110	Alopecurus myosuroides	cDNA
580	TIC110	Amaranthus albus	cDNA
581	TIC110	Amaranthus albus	cDNA
582	TIC110	Amaranthus albus	cDNA
583	TIC110	Amaranthus chlorostachys	cDNA
584	TIC110	Amaranthus graecizans	cDNA
585	TIC110	Amaranthus hybridus	cDNA
586	TIC110	Amaranthus hybridus	cDNA
587	TIC110	Amaranthus lividus	cDNA
588	TIC110	Amaranthus palmeri	cDNA
589	TIC110	Amaranthus palmeri	gDNA
590	TIC110	Amaranthus rudis	cDNA
591	TIC110	Amaranthus rudis	cDNA
592	TIC110	Amaranthus rudis	gDNA
593	TIC110	Amaranthus rudis	gDNA
594	TIC110	Amaranthus rudis	gDNA
595	TIC110	Amaranthus rudis	gDNA
596	TIC110	Amaranthus rudis	gDNA
597	TIC110	Amaranthus rudis	gDNA
598	TIC110	Amaranthus rudis	gDNA
599	TIC110	Amaranthus rudis	gDNA
600	TIC110	Amaranthus rudis	gDNA
601	TIC110	Amaranthus rudis	gDNA
602	TIC110	Amaranthus rudis	gDNA
603	TIC110	Amaranthus spinosus	cDNA
604	TIC110	Amaranthus thunbergii	cDNA
605	TIC110	Amaranthus viridis	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
606	TIC110	Ambrosia artemisiifolia	gDNA
607	TIC110	Ambrosia artemisiifolia	gDNA
608	TIC110	Ambrosia artemisiifolia	gDNA
609	TIC110	Ambrosia artemisiifolia	gDNA
610	TIC110	Ambrosia artemisiifolia	gDNA
611	TIC110	Ambrosia artemisiifolia	gDNA
612	TIC110	Ambrosia artemisiifolia	gDNA
613	TIC110	Ambrosia artemisiifolia	gDNA
614	TIC110	Ambrosia artemisiifolia	gDNA
615	TIC110	Ambrosia trifida	cDNA
616	TIC110	Ambrosia trifida	gDNA
617	TIC110	Ambrosia trifida	gDNA
618	TIC110	Ambrosia trifida	gDNA
619	TIC110	Ambrosia trifida	gDNA
620	TIC110	Ambrosia trifida	gDNA
621	TIC110	Ambrosia trifida	gDNA
622	TIC110	Ambrosia trifida	gDNA
623	TIC110	Ambrosia trifida	gDNA
624	TIC110	Ambrosia trifida	gDNA
625	TIC110	Ambrosia trifida	gDNA
626	TIC110	Ambrosia trifida	gDNA
627	TIC110	Ambrosia trifida	gDNA
628	TIC110	Avena fatua	cDNA
629	TIC110	Chenopodium album	cDNA
630	TIC110	Chenopodium album	cDNA
631	TIC110	Convolvulus arvensis	cDNA
632	TIC110	Convolvulus arvensis	cDNA
633	TIC110	Conyza canadensis	cDNA
634	TIC110	Conyza canadensis	gDNA
635	TIC110	Conyza canadensis	gDNA
636	TIC110	Conyza canadensis	gDNA
637	TIC110	Conyza canadensis	gDNA
638	TIC110	Cyperus esculentus	gDNA
639	TIC110	Cyperus esculentus	gDNA
640	TIC110	Digitaria sanguinalis	cDNA
641	TIC110	Digitaria sanguinalis	cDNA
642	TIC110	Digitaria sanguinalis	cDNA
643	TIC110	Digitaria sanguinalis	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
644	TIC110	Digitaria sanguinalis	gDNA
645	TIC110	Digitaria sanguinalis	gDNA
646	TIC110	Digitaria sanguinalis	gDNA
647	TIC110	Digitaria sanguinalis	gDNA
648	TIC110	Echinochloa colona	cDNA
649	TIC110	Echinochloa crus-galli	cDNA
650	TIC110	Euphorbia heterophylla	cDNA
651	TIC110	Euphorbia heterophylla	gDNA
652	TIC110	Euphorbia heterophylla	gDNA
653	TIC110	Euphorbia heterophylla	gDNA
654	TIC110	Euphorbia heterophylla	gDNA
655	TIC110	Festuca arundinacea	gDNA
656	TIC110	Festuca arundinacea	gDNA
657	TIC110	Festuca arundinacea	gDNA
658	TIC110	Festuca arundinacea	gDNA
659	TIC110	Festuca arundinacea	gDNA
660	TIC110	Festuca arundinacea	gDNA
661	TIC110	Festuca arundinacea	gDNA
662	TIC110	Festuca arundinacea	gDNA
663	TIC110	Ipomoea hederacea	cDNA
664	TIC110	Kochia scoparia	gDNA
665	TIC110	Kochia scoparia	gDNA
666	TIC110	Kochia scoparia	gDNA
667	TIC110	Kochia scoparia	gDNA
668	TIC110	Lolium arundinaceum	gDNA
669	TIC110	Lolium arundinaceum	gDNA
670	TIC110	Lolium arundinaceum	gDNA
671	TIC110	Lolium arundinaceum	gDNA
672	TIC110	Lolium arundinaceum	gDNA
673	TIC110	Lolium arundinaceum	gDNA
674	TIC110	Lolium arundinaceum	gDNA
675	TIC110	Lolium arundinaceum	gDNA
676	TIC110	Lolium multiflorum	cDNA
677	TIC110	Lolium multiflorum	cDNA
678	TIC110	Lolium multiflorum	cDNA
679	TIC110	Lolium multiflorum	gDNA
680	TIC110	Lolium multiflorum	gDNA
681	TIC110	Lolium multiflorum	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
682	TIC110	Lolium multiflorum	gDNA
683	TIC110	Lolium multiflorum	gDNA
684	TIC110	Lolium multiflorum	gDNA
685	TIC110	Lolium multiflorum	gDNA
686	TIC110	Lolium multiflorum	gDNA
687	TIC110	Lolium multiflorum	gDNA
688	TIC110	Lolium multiflorum	gDNA
689	TIC110	Lolium rigidum	gDNA
690	TIC110	Lolium rigidum	gDNA
691	TIC110	Lolium rigidum	gDNA
692	TIC110	Portulaca oleracea	gDNA
693	TIC110	Portulaca oleracea	gDNA
694	TIC110	Portulaca oleracea	gDNA
695	TIC110	Portulaca oleracea	gDNA
696	TIC110	Portulaca oleracea	gDNA
697	TIC110	Portulaca oleracea	gDNA
698	TIC110	Portulaca oleracea	gDNA
699	TIC110	Senna obtusifolia	cDNA
700	TIC110	Setaria viridis	cDNA
701	TIC110	Sorghum halepense	cDNA
702	TIC110	Sorghum halepense	cDNA
703	TIC110	Sorghum halepense	gDNA
704	TIC110	Sorghum halepense	gDNA
705	TIC110	Sorghum halepense	gDNA
706	TIC110	Spirodela polyrrhiza	gDNA
707	TIC110	Taraxacum officinale	gDNA
708	TIC110	Taraxacum officinale	gDNA
709	TIC110	Taraxacum officinale	gDNA
710	TIC110	Taraxacum officinale	gDNA
711	TIC110	Taraxacum officinale	gDNA
712	TIC110	Taraxacum officinale	gDNA
713	TIC110	Trifolium repens	gDNA
714	TIC110	Trifolium repens	gDNA
715	TIC110	Trifolium repens	gDNA
716	TIC110	Trifolium repens	gDNA
717	TIC110	Trifolium repens	gDNA
718	TIC110	Trifolium repens	gDNA
719	TIC110	Trifolium repens	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
720	TIC110	Trifolium repens	gDNA
721	TIC110	Trifolium repens	gDNA
722	TIC110	Xanthium strumarium	cDNA
723	TIC20	Abutilon theophrasti	cDNA
724	TIC20	Abutilon theophrasti	gDNA
725	TIC20	Alopecurus myosuroides	cDNA
726	TIC20	Amaranthus albus	cDNA
727	TIC20	Amaranthus chlorostachys	cDNA
728	TIC20	Amaranthus graecizans	cDNA
729	TIC20	Amaranthus hybridus	cDNA
730	TIC20	Amaranthus lividus	cDNA
731	TIC20	Amaranthus palmeri	cDNA
732	TIC20	Amaranthus palmeri	cDNA
733	TIC20	Amaranthus palmeri	gDNA
734	TIC20	Amaranthus palmeri	gDNA
735	TIC20	Amaranthus rudis	cDNA
736	TIC20	Amaranthus rudis	gDNA
737	TIC20	Amaranthus spinosus	cDNA
738	TIC20	Amaranthus thunbergii	cDNA
739	TIC20	Amaranthus viridis	cDNA
740	TIC20	Ambrosia artemisiifolia	gDNA
741	TIC20	Ambrosia trifida	cDNA
742	TIC20	Ambrosia trifida	gDNA
743	TIC20	Ambrosia trifida	gDNA
744	TIC20	Ambrosia trifida	gDNA
745	TIC20	Chenopodium album	cDNA
746	TIC20	Commelina diffusa	cDNA
747	TIC20	Conyza canadensis	cDNA
748	TIC20	Conyza canadensis	gDNA
749	TIC20	Cyperus esculentus	gDNA
750	TIC20	Digitaria sanguinalis	cDNA
751	TIC20	Echinochloa colona	cDNA
752	TIC20	Echinochloa crus-galli	cDNA
753	TIC20	Euphorbia heterophylla	cDNA
754	TIC20	Euphorbia heterophylla	gDNA
755	TIC20	Festuca arundinacea	gDNA
756	TIC20	Festuca arundinacea	gDNA
757	TIC20	Ipomoea hederacea	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
758	TIC20	Kochia scoparia	gDNA
759	TIC20	Lolium arundinaceum	gDNA
760	TIC20	Lolium multiflorum	cDNA
761	TIC20	Lolium multiflorum	gDNA
762	TIC20	Lolium multiflorum	gDNA
763	TIC20	Lolium rigidum	gDNA
764	TIC20	Portulaca oleracea	gDNA
765	TIC20	Senna obtusifolia	cDNA
766	TIC20	Sorghum halepense	gDNA
767	TIC20	Spirodela polyrrhiza	gDNA
768	TIC20	Taraxacum officinale	gDNA
769	TIC20	Trifolium repens	gDNA
770	TIC20	Xanthium strumarium	cDNA
771	TIC20	Xanthium strumarium	cDNA
772	TIC21	Abutilon theophrasti	cDNA
773	TIC21	Abutilon theophrasti	gDNA
774	TIC21	Abutilon theophrasti	gDNA
775	TIC21	Amaranthus albus	cDNA
776	TIC21	Amaranthus chlorostachys	cDNA
777	TIC21	Amaranthus graecizans	cDNA
778	TIC21	Amaranthus hybridus	cDNA
779	TIC21	Amaranthus lividus	cDNA
780	TIC21	Amaranthus palmeri	cDNA
781	TIC21	Amaranthus palmeri	gDNA
782	TIC21	Amaranthus palmeri	gDNA
783	TIC21	Amaranthus rudis	cDNA
784	TIC21	Amaranthus rudis	gDNA
785	TIC21	Amaranthus rudis	gDNA
786	TIC21	Amaranthus rudis	gDNA
787	TIC21	Amaranthus spinosus	cDNA
788	TIC21	Amaranthus thunbergii	cDNA
789	TIC21	Amaranthus viridis	cDNA
790	TIC21	Ambrosia artemisiifolia	gDNA
791	TIC21	Ambrosia artemisiifolia	gDNA
792	TIC21	Ambrosia artemisiifolia	gDNA
793	TIC21	Ambrosia trifida	cDNA
794	TIC21	Ambrosia trifida	gDNA
795	TIC21	Ambrosia trifida	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
796	TIC21	Ambrosia trifida	gDNA
797	TIC21	Ambrosia trifida	gDNA
798	TIC21	Ambrosia trifida	gDNA
799	TIC21	Ambrosia trifida	gDNA
800	TIC21	Ambrosia trifida	gDNA
801	TIC21	Chenopodium album	cDNA
802	TIC21	Commelina diffusa	cDNA
803	TIC21	Convolvulus arvensis	cDNA
804	TIC21	Conyza canadensis	cDNA
805	TIC21	Conyza canadensis	gDNA
806	TIC21	Cyperus esculentus	gDNA
807	TIC21	Cyperus esculentus	gDNA
808	TIC21	Digitaria sanguinalis	cDNA
809	TIC21	Digitaria sanguinalis	gDNA
810	TIC21	Digitaria sanguinalis	gDNA
811	TIC21	Echinochloa colona	cDNA
812	TIC21	Echinochloa crus-galli	cDNA
813	TIC21	Euphorbia heterophylla	cDNA
814	TIC21	Euphorbia heterophylla	gDNA
815	TIC21	Euphorbia heterophylla	gDNA
816	TIC21	Euphorbia heterophylla	gDNA
817	TIC21	Euphorbia heterophylla	gDNA
818	TIC21	Festuca arundinacea	gDNA
819	TIC21	Ipomoea hederacea	cDNA
820	TIC21	Kochia scoparia	gDNA
821	TIC21	Lolium arundinaceum	gDNA
822	TIC21	Lolium arundinaceum	gDNA
823	TIC21	Lolium rigidum	gDNA
824	TIC21	Lolium rigidum	gDNA
825	TIC21	Lolium rigidum	gDNA
826	TIC21	Portulaca oleracea	gDNA
827	TIC21	Portulaca oleracea	gDNA
828	TIC21	Portulaca oleracea	gDNA
829	TIC21	Senna obtusifolia	cDNA
830	TIC21	Setaria viridis	cDNA
831	TIC21	Sorghum halepense	cDNA
832	TIC21	Sorghum halepense	gDNA
833	TIC21	Sorghum halepense	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
834	TIC21	Spirodela polyrrhiza	gDNA
835	TIC21	Taraxacum officinale	gDNA
836	TIC21	Taraxacum officinale	gDNA
837	TIC21	Trifolium repens	gDNA
838	TIC21	Trifolium repens	gDNA
839	TIC21	Xanthium strumarium	cDNA
840	TIC21	Xanthium strumarium	cDNA
841	TIC40	Abutilon theophrasti	cDNA
842	TIC40	Abutilon theophrasti	gDNA
843	TIC40	Abutilon theophrasti	gDNA
844	TIC40	Abutilon theophrasti	gDNA
845	TIC40	Abutilon theophrasti	gDNA
846	TIC40	Abutilon theophrasti	gDNA
847	TIC40	Abutilon theophrasti	gDNA
848	TIC40	Abutilon theophrasti	gDNA
849	TIC40	Abutilon theophrasti	gDNA
850	TIC40	Abutilon theophrasti	gDNA
851	TIC40	Alopecurus myosuroides	cDNA
852	TIC40	Amaranthus albus	cDNA
853	TIC40	Amaranthus albus	cDNA
854	TIC40	Amaranthus chlorostachys	cDNA
855	TIC40	Amaranthus graecizans	cDNA
856	TIC40	Amaranthus hybridus	cDNA
857	TIC40	Amaranthus lividus	cDNA
858	TIC40	Amaranthus palmeri	cDNA
859	TIC40	Amaranthus palmeri	gDNA
860	TIC40	Amaranthus palmeri	gDNA
861	TIC40	Amaranthus palmeri	gDNA
862	TIC40	Amaranthus palmeri	gDNA
863	TIC40	Amaranthus palmeri	gDNA
864	TIC40	Amaranthus rudis	cDNA
865	TIC40	Amaranthus rudis	gDNA
866	TIC40	Amaranthus rudis	gDNA
867	TIC40	Amaranthus rudis	gDNA
868	TIC40	Amaranthus rudis	gDNA
869	TIC40	Amaranthus rudis	gDNA
870	TIC40	Amaranthus spinosus	cDNA
871	TIC40	Amaranthus spinosus	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
872	TIC40	Amaranthus thunbergii	cDNA
873	TIC40	Amaranthus viridis	cDNA
874	TIC40	Ambrosia artemisiifolia	gDNA
875	TIC40	Ambrosia artemisiifolia	gDNA
876	TIC40	Ambrosia trifida	cDNA
877	TIC40	Ambrosia trifida	gDNA
878	TIC40	Ambrosia trifida	gDNA
879	TIC40	Ambrosia trifida	gDNA
880	TIC40	Ambrosia trifida	gDNA
881	TIC40	Ambrosia trifida	gDNA
882	TIC40	Ambrosia trifida	gDNA
883	TIC40	Chenopodium album	cDNA
884	TIC40	Commelina diffusa	cDNA
885	TIC40	Conyza canadensis	cDNA
886	TIC40	Conyza canadensis	gDNA
887	TIC40	Cyperus esculentus	gDNA
888	TIC40	Echinochloa colona	cDNA
889	TIC40	Echinochloa crus-galli	cDNA
890	TIC40	Euphorbia heterophylla	cDNA
891	TIC40	Euphorbia heterophylla	gDNA
892	TIC40	Euphorbia heterophylla	gDNA
893	TIC40	Euphorbia heterophylla	gDNA
894	TIC40	Euphorbia heterophylla	gDNA
895	TIC40	Festuca arundinacea	gDNA
896	TIC40	Ipomoea hederacea	cDNA
897	TIC40	Kochia scoparia	gDNA
898	TIC40	Kochia scoparia	gDNA
899	TIC40	Lolium arundinaceum	gDNA
900	TIC40	Lolium arundinaceum	gDNA
901	TIC40	Lolium rigidum	gDNA
902	TIC40	Lolium rigidum	gDNA
903	TIC40	Portulaca oleracea	gDNA
904	TIC40	Portulaca oleracea	gDNA
905	TIC40	Portulaca oleracea	gDNA
906	TIC40	Senna obtusifolia	cDNA
907	TIC40	Sorghum halepense	cDNA
908	TIC40	Sorghum halepense	gDNA
909	TIC40	Spirodela polyrrhiza	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
910	TIC40	Taraxacum officinale	gDNA
911	TIC40	Trifolium repens	gDNA
912	TIC40	Xanthium strumarium	cDNA
913	SPP	Abutilon theophrasti	cDNA
914	SPP	Abutilon theophrasti	cDNA
915	SPP	Abutilon theophrasti	gDNA
916	SPP	Abutilon theophrasti	gDNA
917	SPP	Abutilon theophrasti	gDNA
918	SPP	Abutilon theophrasti	gDNA
919	SPP	Abutilon theophrasti	gDNA
920	SPP	Abutilon theophrasti	gDNA
921	SPP	Abutilon theophrasti	gDNA
922	SPP	Abutilon theophrasti	gDNA
923	SPP	Abutilon theophrasti	gDNA
924	SPP	Abutilon theophrasti	gDNA
925	SPP	Abutilon theophrasti	gDNA
926	SPP	Abutilon theophrasti	gDNA
927	SPP	Abutilon theophrasti	gDNA
928	SPP	Abutilon theophrasti	gDNA
929	SPP	Abutilon theophrasti	gDNA
930	SPP	Alopecurus myosuroides	cDNA
931	SPP	Alopecurus myosuroides	cDNA
932	SPP	Alopecurus myosuroides	cDNA
933	SPP	Amaranthus albus	cDNA
934	SPP	Amaranthus albus	cDNA
935	SPP	Amaranthus albus	cDNA
936	SPP	Amaranthus chlorostachys	cDNA
937	SPP	Amaranthus chlorostachys	cDNA
938	SPP	Amaranthus chlorostachys	cDNA
939	SPP	Amaranthus graecizans	cDNA
940	SPP	Amaranthus graecizans	cDNA
941	SPP	Amaranthus hybridus	cDNA
942	SPP	Amaranthus hybridus	cDNA
943	SPP	Amaranthus hybridus	cDNA
944	SPP	Amaranthus hybridus	cDNA
945	SPP	Amaranthus lividus	cDNA
946	SPP	Amaranthus lividus	cDNA
947	SPP	Amaranthus lividus	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
948	SPP	Amaranthus lividus	cDNA
949	SPP	Amaranthus lividus	cDNA
950	SPP	Amaranthus palmeri	cDNA
951	SPP	Amaranthus palmeri	gDNA
952	SPP	Amaranthus palmeri	gDNA
953	SPP	Amaranthus palmeri	gDNA
954	SPP	Amaranthus palmeri	gDNA
955	SPP	Amaranthus palmeri	gDNA
956	SPP	Amaranthus palmeri	gDNA
957	SPP	Amaranthus rudis	cDNA
958	SPP	Amaranthus rudis	cDNA
959	SPP	Amaranthus rudis	gDNA
960	SPP	Amaranthus rudis	gDNA
961	SPP	Amaranthus rudis	gDNA
962	SPP	Amaranthus rudis	gDNA
963	SPP	Amaranthus rudis	gDNA
964	SPP	Amaranthus rudis	gDNA
965	SPP	Amaranthus rudis	gDNA
966	SPP	Amaranthus rudis	gDNA
967	SPP	Amaranthus spinosus	cDNA
968	SPP	Amaranthus spinosus	cDNA
969	SPP	Amaranthus spinosus	cDNA
970	SPP	Amaranthus thunbergii	cDNA
971	SPP	Amaranthus thunbergii	cDNA
972	SPP	Amaranthus thunbergii	cDNA
973	SPP	Amaranthus thunbergii	cDNA
974	SPP	Amaranthus viridis	cDNA
975	SPP	Amaranthus viridis	cDNA
976	SPP	Amaranthus viridis	cDNA
977	SPP	Ambrosia artemisiifolia	gDNA
978	SPP	Ambrosia artemisiifolia	gDNA
979	SPP	Ambrosia artemisiifolia	gDNA
980	SPP	Ambrosia artemisiifolia	gDNA
981	SPP	Ambrosia artemisiifolia	gDNA
982	SPP	Ambrosia artemisiifolia	gDNA
983	SPP	Ambrosia artemisiifolia	gDNA
984	SPP	Ambrosia artemisiifolia	gDNA
985	SPP	Ambrosia artemisiifolia	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
986	SPP	Ambrosia artemisiifolia	gDNA
987	SPP	Ambrosia artemisiifolia	gDNA
988	SPP	Ambrosia artemisiifolia	gDNA
989	SPP	Ambrosia artemisiifolia	gDNA
990	SPP	Ambrosia artemisiifolia	gDNA
991	SPP	Ambrosia artemisiifolia	gDNA
992	SPP	Ambrosia trifida	cDNA
993	SPP	Ambrosia trifida	cDNA
994	SPP	Ambrosia trifida	cDNA
995	SPP	Ambrosia trifida	cDNA
996	SPP	Ambrosia trifida	cDNA
997	SPP	Ambrosia trifida	gDNA
998	SPP	Ambrosia trifida	gDNA
999	SPP	Ambrosia trifida	gDNA
1000	SPP	Ambrosia trifida	gDNA
1001	SPP	Ambrosia trifida	gDNA
1002	SPP	Ambrosia trifida	gDNA
1003	SPP	Ambrosia trifida	gDNA
1004	SPP	Ambrosia trifida	gDNA
1005	SPP	Ambrosia trifida	gDNA
1006	SPP	Ambrosia trifida	gDNA
1007	SPP	Ambrosia trifida	gDNA
1008	SPP	Ambrosia trifida	gDNA
1009	SPP	Ambrosia trifida	gDNA
1010	SPP	Ambrosia trifida	gDNA
1011	SPP	Ambrosia trifida	gDNA
1012	SPP	Ambrosia trifida	gDNA
1013	SPP	Ambrosia trifida	gDNA
1014	SPP	Ambrosia trifida	gDNA
1015	SPP	Ambrosia trifida	gDNA
1016	SPP	Ambrosia trifida	gDNA
1017	SPP	Ambrosia trifida	gDNA
1018	SPP	Ambrosia trifida	gDNA
1019	SPP	Avena fatua	cDNA
1020	SPP	Chenopodium album	cDNA
1021	SPP	Chenopodium album	cDNA
1022	SPP	Convolvulus arvensis	cDNA
1023	SPP	Conyza canadensis	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
1024	SPP	Conyza canadensis	gDNA
1025	SPP	Cyperus esculentus	gDNA
1026	SPP	Cyperus esculentus	gDNA
1027	SPP	Digitaria sanguinalis	cDNA
1028	SPP	Digitaria sanguinalis	cDNA
1029	SPP	Digitaria sanguinalis	gDNA
1030	SPP	Digitaria sanguinalis	gDNA
1031	SPP	Digitaria sanguinalis	gDNA
1032	SPP	Digitaria sanguinalis	gDNA
1033	SPP	Echinochloa colona	cDNA
1034	SPP	Echinochloa colona	cDNA
1035	SPP	Echinochloa crus-galli	cDNA
1036	SPP	Euphorbia heterophylla	cDNA
1037	SPP	Euphorbia heterophylla	cDNA
1038	SPP	Euphorbia heterophylla	cDNA
1039	SPP	Euphorbia heterophylla	gDNA
1040	SPP	Euphorbia heterophylla	gDNA
1041	SPP	Euphorbia heterophylla	gDNA
1042	SPP	Euphorbia heterophylla	gDNA
1043	SPP	Euphorbia heterophylla	gDNA
1044	SPP	Euphorbia heterophylla	gDNA
1045	SPP	Festuca arundinacea	gDNA
1046	SPP	Festuca arundinacea	gDNA
1047	SPP	Festuca arundinacea	gDNA
1048	SPP	Festuca arundinacea	gDNA
1049	SPP	Festuca arundinacea	gDNA
1050	SPP	Festuca arundinacea	gDNA
1051	SPP	Festuca arundinacea	gDNA
1052	SPP	Festuca arundinacea	gDNA
1053	SPP	Festuca arundinacea	gDNA
1054	SPP	Festuca arundinacea	gDNA
1055	SPP	Festuca arundinacea	gDNA
1056	SPP	Ipomoea hederacea	cDNA
1057	SPP	Ipomoea hederacea	cDNA
1058	SPP	Kochia scoparia	gDNA
1059	SPP	Kochia scoparia	gDNA
1060	SPP	Kochia scoparia	gDNA
1061	SPP	Kochia scoparia	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_TY P E
1062	SPP	Kochia scoparia	gDNA
1063	SPP	Kochia scoparia	gDNA
1064	SPP	Kochia scoparia	gDNA
1065	SPP	Kochia scoparia	gDNA
1066	SPP	Kochia scoparia	gDNA
1067	SPP	Lolium arundinaceum	gDNA
1068	SPP	Lolium arundinaceum	gDNA
1069	SPP	Lolium arundinaceum	gDNA
1070	SPP	Lolium arundinaceum	gDNA
1071	SPP	Lolium arundinaceum	gDNA
1072	SPP	Lolium arundinaceum	gDNA
1073	SPP	Lolium arundinaceum	gDNA
1074	SPP	Lolium arundinaceum	gDNA
1075	SPP	Lolium arundinaceum	gDNA
1076	SPP	Lolium arundinaceum	gDNA
1077	SPP	Lolium arundinaceum	gDNA
1078	SPP	Lolium arundinaceum	gDNA
1079	SPP	Lolium arundinaceum	gDNA
1080	SPP	Lolium arundinaceum	gDNA
1081	SPP	Lolium arundinaceum	gDNA
1082	SPP	Lolium multiflorum	cDNA
1083	SPP	Lolium multiflorum	cDNA
1084	SPP	Lolium multiflorum	gDNA
1085	SPP	Lolium multiflorum	gDNA
1086	SPP	Lolium multiflorum	gDNA
1087	SPP	Lolium multiflorum	gDNA
1088	SPP	Lolium multiflorum	gDNA
1089	SPP	Lolium multiflorum	gDNA
1090	SPP	Lolium multiflorum	gDNA
1091	SPP	Lolium multiflorum	gDNA
1092	SPP	Lolium rigidum	gDNA
1093	SPP	Lolium rigidum	gDNA
1094	SPP	Lolium rigidum	gDNA
1095	SPP	Lolium rigidum	gDNA
1096	SPP	Lolium rigidum	gDNA
1097	SPP	Portulaca oleracea	gDNA
1098	SPP	Portulaca oleracea	gDNA
1099	SPP	Portulaca oleracea	gDNA

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(continued)

SEQ ID NO	GENE	SPECIES	SEQ_TYP E
1100	SPP	Portulaca oleracea	gDNA
1101	SPP	Portulaca oleracea	gDNA
1102	SPP	Portulaca oleracea	gDNA
1103	SPP	Portulaca oleracea	gDNA
1104	SPP	Portulaca oleracea	gDNA
1105	SPP	Portulaca oleracea	gDNA
1106	SPP	Senna obtusifolia	cDNA
1107	SPP	Sorghum halepense	cDNA
1108	SPP	Sorghum halepense	gDNA
1109	SPP	Sorghum halepense	gDNA
1110	SPP	Sorghum halepense	gDNA
1111	SPP	Sorghum halepense	gDNA
1112	SPP	Sorghum halepense	gDNA
1113	SPP	Spirodela polyrrhiza	gDNA
1114	SPP	Taraxacum officinale	gDNA
1115	SPP	Taraxacum officinale	gDNA
1116	SPP	Taraxacum officinale	gDNA
1117	SPP	Taraxacum officinale	gDNA
1118	SPP	Taraxacum officinale	gDNA
1119	SPP	Trifolium repens	gDNA
1120	SPP	Trifolium repens	gDNA
1121	SPP	Trifolium repens	gDNA
1122	SPP	Trifolium repens	gDNA
1123	SPP	Trifolium repens	gDNA
1124	SPP	Trifolium repens	gDNA
1125	SPP	Trifolium repens	gDNA
1126	SPP	Trifolium repens	gDNA
1127	SPP	Trifolium repens	gDNA
1128	SPP	Xanthium strumarium	cDNA
1129	SPP	Xanthium strumarium	cDNA
1130	SPP	Xanthium strumarium	cDNA
1131	TIC100	Abutilon theophrasti	cDNA
1132	TIC100	Abutilon theophrasti	gDNA
1133	TIC100	Abutilon theophrasti	gDNA
1134	TIC100	Abutilon theophrasti	gDNA
1135	TIC100	Abutilon theophrasti	gDNA
1136	TIC100	Amaranthus chlorostachys	cDNA
1137	TIC100	Amaranthus graecizans	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
1138	TIC100	Amaranthus hybridus	cDNA
1139	TIC100	Amaranthus hybridus	cDNA
1140	TIC100	Amaranthus lividus	cDNA
1141	TIC100	Amaranthus lividus	cDNA
1142	TIC100	Amaranthus palmeri	cDNA
1143	TIC100	Amaranthus palmeri	gDNA
1144	TIC100	Amaranthus palmeri	gDNA
1145	TIC100	Amaranthus rudis	cDNA
1146	TIC100	Amaranthus rudis	cDNA
1147	TIC100	Amaranthus rudis	gDNA
1148	TIC100	Amaranthus rudis	gDNA
1149	TIC100	Amaranthus rudis	gDNA
1150	TIC100	Amaranthus rudis	gDNA
1151	TIC100	Amaranthus rudis	gDNA
1152	TIC100	Amaranthus rudis	gDNA
1153	TIC100	Amaranthus rudis	gDNA
1154	TIC100	Amaranthus rudis	gDNA
1155	TIC100	Amaranthus rudis	gDNA
1156	TIC100	Amaranthus rudis	gDNA
1157	TIC100	Amaranthus spinosus	cDNA
1158	TIC100	Amaranthus thunbergii	cDNA
1159	TIC100	Amaranthus thunbergii	cDNA
1160	TIC100	Amaranthus viridis	cDNA
1161	TIC100	Amaranthus viridis	cDNA
1162	TIC100	Ambrosia artemisiifolia	gDNA
1163	TIC100	Ambrosia artemisiifolia	gDNA
1164	TIC100	Ambrosia artemisiifolia	gDNA
1165	TIC100	Ambrosia artemisiifolia	gDNA
1166	TIC100	Ambrosia artemisiifolia	gDNA
1167	TIC100	Ambrosia trifida	cDNA
1168	TIC100	Ambrosia trifida	gDNA
1169	TIC100	Ambrosia trifida	gDNA
1170	TIC100	Ambrosia trifida	gDNA
1171	TIC100	Ambrosia trifida	gDNA
1172	TIC100	Ambrosia trifida	gDNA
1173	TIC100	Ambrosia trifida	gDNA
1174	TIC100	Ambrosia trifida	gDNA
1175	TIC100	Chenopodium album	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
1176	TIC100	Chenopodium album	cDNA
1177	TIC100	Chenopodium album	cDNA
1178	TIC100	Conyza canadensis	cDNA
1179	TIC100	Conyza canadensis	gDNA
1180	TIC100	Digitaria sanguinalis	cDNA
1181	TIC100	Digitaria sanguinalis	gDNA
1182	TIC100	Digitaria sanguinalis	gDNA
1183	TIC100	Digitaria sanguinalis	gDNA
1184	TIC100	Digitaria sanguinalis	gDNA
1185	TIC100	Digitaria sanguinalis	gDNA
1186	TIC100	Euphorbia heterophylla	cDNA
1187	TIC100	Euphorbia heterophylla	gDNA
1188	TIC100	Ipomoea hederacea	cDNA
1189	TIC100	Kochia scoparia	gDNA
1190	TIC100	Kochia scoparia	gDNA
1191	TIC100	Kochia scoparia	gDNA
1192	TIC100	Kochia scoparia	gDNA
1193	TIC100	Portulaca oleracea	gDNA
1194	TIC100	Portulaca oleracea	gDNA
1195	TIC100	Portulaca oleracea	gDNA
1196	TIC100	Senna obtusifolia	cDNA
1197	TIC100	Spirodela polyrrhiza	gDNA
1198	TIC100	Taraxacum officinale	gDNA
1199	TIC100	Taraxacum officinale	gDNA
1200	TIC100	Taraxacum officinale	gDNA
1201	TIC100	Taraxacum officinale	gDNA
1202	TIC100	Trifolium repens	gDNA
1203	TIC100	Trifolium repens	gDNA
1204	TIC100	Trifolium repens	gDNA
1205	TIC100	Trifolium repens	gDNA
1206	TIC100	Trifolium repens	gDNA
1207	TIC100	Xanthium strumarium	cDNA
1208	TIC56	Abutilon theophrasti	cDNA
1209	TIC56	Abutilon theophrasti	gDNA
1210	TIC56	Abutilon theophrasti	gDNA
1211	TIC56	Abutilon theophrasti	gDNA
1212	TIC56	Abutilon theophrasti	gDNA
1213	TIC56	Amaranthus graecizans	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
1214	TIC56	Amaranthus graecizans	cDNA
1215	TIC56	Amaranthus hybridus	cDNA
1216	TIC56	Amaranthus lividus	cDNA
1217	TIC56	Amaranthus palmeri	cDNA
1218	TIC56	Amaranthus palmeri	gDNA
1219	TIC56	Amaranthus palmeri	gDNA
1220	TIC56	Amaranthus rudis	cDNA
1221	TIC56	Amaranthus rudis	gDNA
1222	TIC56	Amaranthus rudis	gDNA
1223	TIC56	Amaranthus rudis	gDNA
1224	TIC56	Amaranthus rudis	gDNA
1225	TIC56	Amaranthus rudis	gDNA
1226	TIC56	Amaranthus rudis	gDNA
1227	TIC56	Amaranthus rudis	gDNA
1228	TIC56	Amaranthus spinosus	cDNA
1229	TIC56	Amaranthus spinosus	cDNA
1230	TIC56	Amaranthus thunbergii	cDNA
1231	TIC56	Amaranthus viridis	cDNA
1232	TIC56	Amaranthus viridis	cDNA
1233	TIC56	Ambrosia artemisiifolia	gDNA
1234	TIC56	Ambrosia artemisiifolia	gDNA
1235	TIC56	Ambrosia artemisiifolia	gDNA
1236	TIC56	Ambrosia artemisiifolia	gDNA
1237	TIC56	Ambrosia trifida	cDNA
1238	TIC56	Ambrosia trifida	gDNA
1239	TIC56	Ambrosia trifida	gDNA
1240	TIC56	Ambrosia trifida	gDNA
1241	TIC56	Ambrosia trifida	gDNA
1242	TIC56	Chenopodium album	cDNA
1243	TIC56	Conyza canadensis	cDNA
1244	TIC56	Conyza canadensis	cDNA
1245	TIC56	Conyza canadensis	gDNA
1246	TIC56	Digitaria sanguinalis	cDNA
1247	TIC56	Digitaria sanguinalis	gDNA
1248	TIC56	Digitaria sanguinalis	gDNA
1249	TIC56	Euphorbia heterophylla	cDNA
1250	TIC56	Euphorbia heterophylla	gDNA
1251	TIC56	Euphorbia heterophylla	gDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
1252	TIC56	Euphorbia heterophylla	gDNA
1253	TIC56	Ipomoea hederacea	cDNA
1254	TIC56	Kochia scoparia	gDNA
1255	TIC56	Portulaca oleracea	gDNA
1256	TIC56	Portulaca oleracea	gDNA
1257	TIC56	Senna obtusifolia	cDNA
1258	TIC56	Spirodela polyrrhiza	gDNA
1259	TIC56	Taraxacum officinale	gDNA
1260	TIC56	Trifolium repens	gDNA
1261	TIC56	Trifolium repens	gDNA
1262	TIC56	Xanthium strumarium	cDNA
1263	TIC56	Xanthium strumarium	cDNA
1584	HSP70	Amaranthus palmeri	cDNA
1585	HSP70	Amaranthus palmeri	gDNA
1586	HSP70-1	Amaranthus palmeri	cDNA
1587	HSP70-1	Amaranthus palmeri	cDNA
1588	HSP70-1	Amaranthus palmeri	gDNA
1589	HSP70-1	Amaranthus palmeri	gDNA
1590	HSP70T-1	Amaranthus palmeri	cDNA
1591	HSP70T-1	Amaranthus palmeri	gDNA
1592	HSP70T-1	Amaranthus palmeri	gDNA
1593	HSP70T-2	Amaranthus palmeri	cDNA
1594	HSP70T-2	Amaranthus palmeri	cDNA
1595	HSP70T-2	Amaranthus palmeri	gDNA
1596	HSP93III	Amaranthus palmeri	gDNA
1597	HSP93IIIb	Amaranthus palmeri	cDNA
1598	HSP93IIIb	Amaranthus palmeri	gDNA
1599	HSP93IIIb	Amaranthus palmeri	gDNA
1600	HSP93IIIb	Amaranthus palmeri	gDNA
1601	HSP93IIIb	Amaranthus palmeri	cDNA
1602	HSP93IIIb	Amaranthus palmeri	cDNA
1603	HSP93V	Amaranthus palmeri	cDNA
1604	HSP93V	Amaranthus palmeri	cDNA
1605	HSP93V	Amaranthus palmeri	cDNA
1606	HSP93V	Amaranthus palmeri	gDNA
1607	HSP93V	Amaranthus palmeri	gDNA
1608	HSP93V	Amaranthus palmeri	gDNA
1609	TIC22-like	Amaranthus palmeri	cDNA

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SEQ ID NO	GENE	SPECIES	SEQ_ TYPE
1610	TIC22-like	Amaranthus palmeri	gDNA
1611	TIC22-like1	Amaranthus palmeri	cDNA
1612	TIC22-like1	Amaranthus palmeri	gDNA
1613	TIC22-like2	Amaranthus palmeri	cDNA
1614	TIC22-like2	Amaranthus palmeri	gDNA
1615	TIC22-like2	Amaranthus palmeri	gDNA
1616	TIC55II	Amaranthus palmeri	cDNA
1617	TIC55II	Amaranthus palmeri	cDNA
1618	TIC55II	Amaranthus palmeri	gDNA
1619	TIC55II	Amaranthus palmeri	gDNA
1620	TIC55IV	Amaranthus palmeri	cDNA
1621	TIC55IV	Amaranthus palmeri	gDNA
1622	TIC55IV	Amaranthus palmeri	gDNA
1623	TIC55IV	Amaranthus palmeri	gDNA
1624	TIC62	Amaranthus palmeri	cDNA
1625	TIC62	Amaranthus palmeri	gDNA
1626	TIC62	Amaranthus palmeri	gDNA
1627	TIC62	Amaranthus palmeri	gDNA
1628	TOC64I	Amaranthus palmeri	cDNA
1629	TOC64I	Amaranthus palmeri	gDNA
1630	TOC64III	Amaranthus palmeri	cDNA
1631	TOC64III	Amaranthus palmeri	gDNA
1632	TOC64III	Amaranthus palmeri	gDNA
1633	TOC64V	Amaranthus palmeri	cDNA
1634	TOC64V	Amaranthus palmeri	cDNA
1635	TOC64V	Amaranthus palmeri	cDNA
1636	TOC64V	Amaranthus palmeri	gDNA
1637	TOC64V	Amaranthus palmeri	gDNA
1638	TOC64V	Amaranthus palmeri	gDNA

Example 2. Polynucleotide molecules homologous in weed species

[0057] The gene sequences and fragments of SEQ ID NO: 1-1263 were compared and 25-mers of contiguous polynucleotides were identified that have homology across the various gene sequences for each set of chloroplast protein import system genes and across the various target weed species. The purpose is to identify trigger polynucleotide molecules that are useful alone or in combination with a herbicide to provide enhanced weed control across a range of weed species, including glyphosate and other herbicide resistant weed biotypes. The method can be applied to any set of target gene sequences to identify trigger polynucleotides common to more than one weed species. The method can further be applied to identify medium length trigger polynucleotides, for example 26-mer, 27-mer, 28-mer, 29-mer, 30-mer, 31-mer, 32-mer, 33-mer, 34-mer, 35-mer, 36-mer, 37-mer, 38-mer, 39-mer, 40-mer, 41-mer, 42-mer, 43-mer, 44-mer, 45-mer, 46-mer, 47-mer, 48-mer, 49-mer, 50-mer, 51-mer, 52-mer, 53-mer, 54-mer, 55-mer, 56-mer, 57-mer, 58-mer, 59-mer, 60-mer, common to more than one weed species.

[0058] The sequences shown in Table 2 represent the 25-mers of the respective gene sequences in SEQ ID NO: 1-1263 that have homology to eight or more weed species. It is contemplated that additional 25-mers can be selected from the gene sequences that are specific for a single weed species or a few weeds species within a genus or trigger polynucleotide molecules that are at least 19 contiguous nucleotides and at least 85 percent identical to a gene sequence of SEQ ID NO: 1-1263. The 25-mer oligonucleotides are combined into a 5-10 polynucleotide pooled set and tested for efficacy against the broadest range of weed species in which the polynucleotide is essentially identical or essentially complementary to a gene sequence in the genome of the treated weed species. Efficacious sets are divided into smaller sets of 2-3 polynucleotides or tested individually for efficacy. Each polynucleotide set is prepared with the transfer agent and applied to a plant or a field of plants in combination with a herbicide, or followed by a herbicide treatment one to three days after the oligonucleotide application, to determine the effect in the plant's susceptibility to the herbicide. The effect is measured as stunting the growth and/or killing of the plant and is measured 8-14 days or 21 days after treatment with the polynucleotide set and the herbicide.

Table 2. Plant chloroplast import system gene trigger polynucleotides.

SEQ ID NO	Seq	Gene	# Species	Species
1264	TTTGGTAATGAA TGTGGTTGAGCG T	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1265	TTGGTAATGAAT GTGGTTGAGCGT G	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1266	TTGATTTGGTAA TGAATGTGGTTG A	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1267	TGGTAATGAATG TGGTTGAGCGTG T	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1268	TGGATTGAAGGT GATGATAAGCGT A	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1269	TGATTTGGTAAT GAATGTGGTTGA G	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1270	TCACACGCTCAA CCACATTCATTA C	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1271	TCAACCACATTC ATTACCAAATCA A	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1272	TACGCTTATCAT CACCTTCAATCC A	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album

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SEQ ID NO	Seq	Gene	# Species	Species
1273	TAATGAATGTGG TTGAGCGTGTGA G	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1274	GTTGATTTGGTA ATGAATGTGGTT G	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1275	GTACGCTTATCA TCACCTTCAATC C	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1276	GTAATGAATGTG GTTGAGCGTGTG A	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1277	GGTAATGAATGT GGTTGAGCGTGT G	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1278	GGTAAAGTTGAT TTGGTAATGAAT G	OEP80	8	Abutilon theophrasti, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis
1279	GGATTGAAGGTG ATGATAAGCGTA C	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1280	GCTCAACCACAT TCATTACCAAAT C	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1281	GATTTGGTAATG AATGTGGTTGAG C	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1282	CTCACACGCTCA ACCACATTCATT A	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album
1283	CTCAACCACATT CATTACCAAATC A	OEP80	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus viridis, Chenopodium album

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(continued)

SEQ ID NO	Seq	Gene	# Species	Species
1284	TTTCCACCCTCA TCTTTGATCTCCT	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1285	TTTAGCTTCATC GAGTTTCGGGTC T	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1286	TTCTGGTACGGC TACATGATTCAT G	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1287	TTCCACCCTCAT CTTTGATCTCCT C	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1288	TTCCACATGAAT CATGTAGCCGTA C	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1289	TTCATCGAGTTT CGGGTCTGTTTC A	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1290	TTAGCTTCATCG AGTTTCGGGTCT G	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1291	TTACTTCTGGTA CGGCTACATGAT T	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1292	TGGTACGGCTAC ATGATTCATGTG G	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1293	TGGAAGCATGGC AGAATGCATGGT T	TIC100	9	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Conyza canadensis
1294	TGATTTAGCTTC ATCGAGTTTCGG G	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1295	TGATGATTTAGC TTCATCGAGTTT C	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1296	TGATGATGATTT AGCTTCATCGAG T	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1297	TGATGATGATGA TTTAGCTTCATC G	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1298	TGATGATGATGA TGATTTAGCTTC A	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1299	TGAATCATGTAG CCGTACCAGAAG T	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1300	TGAAGCTAAATC ATCATCATCATC A	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1301	TGAAACAGACCC GAAACTCGATGA A	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1302	TCTGGTACGGCT ACATGATTCATG T	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1303	TCTGAAACAGAC CCGAAACTCGAT G	TIC100	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1304	AGCTTCTGAAAT GCCCCGACGCTGT T	TIC110	12	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Ambrosia trifida, Conyza canadensis, Digitaria sanguinalis, Xanthium strumarium

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SEQ ID NO	Seq	Gene	# Species	Species
1305	AACAGCGTCGGG CATTTCAGAAGC T	TIC110	12	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Ambrosia trifida, Conyza canadensis, Digitaria sanguinalis, Xanthium strumarium
1306	TGTGCTGCTTTC CTTACAGATGCT T	TIC110	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1307	GTGCTGCTTTCC TTACAGATGCTT T	TIC110	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1308	GCTTCTGAAATG CCCGACGCTGTT C	TIC110	10	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Ambrosia trifida, Conyza canadensis
1309	GAACAGCGTCGG GCATTTCAGAAG C	TIC110	10	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Ambrosia trifida, Conyza canadensis
1310	AAGCATCTGTAA GGAAAGCAGCA CA	TIC110	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1311	AAAGCATCTGTA AGGAAAGCAGC AC	TIC110	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1312	TTTGAGCATATT CTGCAGGCAGCC C	TIC110	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1313	TTTCTCTGCCTC AATAAAGCCACG G	TIC110	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1314	TTTCAATGGCAG CAGCCATCTTTG A	TIC110	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1315	TTTAGACAGCAG GCCGAGGTCATT T	TIC110	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1316	TTGGTTCAAGCC GTGGCTTTATTG A	TIC110	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1317	TTGCTGAAGCTT CTGTCGATATAT T	TIC110	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1318	TTGCCAGCAATT GACATAGCAGCT T	TIC110	9	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus thunbergii, Amaranthus viridis
1319	TTCTGTCGATAT ATTTCTTCATGG A	TIC110	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1320	TTCTCTGCCTCA ATAAAGCCACGG C	TIC110	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1321	TTCAATGGCAGC AGCCATCTTTGA A	TIC110	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1322	TTCAAGCCGTGG CTTTATTGAGGC A	TIC110	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1323	TTCAAAGATGGC TGCTGCCATTGA A	TIC110	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1324	TGCTGCATATAT CCAAATTCCATA T	TIC20	11	Abutilon theophrasti, Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1325	TCATATGGAATT TGGATATATGCA G	TIC20	11	Abutilon theophrasti, Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1326	TATGGAATTTGG ATATATGCAGCA T	TIC20	11	Abutilon theophrasti, Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1327	GCTGCATATATC CAAATTCCATAT G	TIC20	11	Abutilon theophrasti, Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1328	GATGCTGCATAT ATCCAAATTCCA T	TIC20	11	Abutilon theophrasti, Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1329	CTGCATATATCC AAATTCCATATG A	TIC20	11	Abutilon theophrasti, Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1330	CATATGGAATTT GGATATATGCAG C	TIC20	11	Abutilon theophrasti, Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1331	ATGGAATTTGGA TATATGCAGCAT C	TIC20	11	Abutilon theophrasti, Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1332	ATGCTGCATATA TCCAAATTCCAT A	TIC20	11	Abutilon theophrasti, Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1333	ATATGGAATTTG GATATATGCAGC A	TIC20	11	Abutilon theophrasti, Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1334	TTTGTGCTTACC TTGGGATCGTGA G	TIC20	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1335	TTTGTATGCGAT GCTGCATATATC C	TIC20	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1336	TTTGGATATATG CAGCATCGCATA C	TIC20	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1337	TTTGCAGGTTGT TGGTACTGTCAG T	TIC20	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1338	TTTCTCCTCACG ATCCCAAGGTAA G	TIC20	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1339	TTGTTGGTACTG TCAGTCGTTGGC T	TIC20	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1340	TTGTGCTTACCT TGGGATCGTGAG G	TIC20	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1341	TTGTATGCGATG CTGCATATATCC A	TIC20	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1342	TTGGTACTGTCA GTCGTTGGCTGC C	TIC20	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1343	TTGGGATCGTGA GGAGAAAGGAG TG	TIC20	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1344	TTTGGAATTGTT GCGATCAGTGAC A	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1345	TTTGAATCTTCTT GGTATGGGCTCT	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1346	TTTCCTCTTTGG AATTGTTGCGAT C	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1347	TTTATTGCTGTT GATAATTGTGCA G	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1348	TTGTTGCGATCA GTGACATCACCT A	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1349	TTGGTATGGGCT CTGCGGTCTTGG G	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1350	TTGGAATTGTTG CGATCAGTGACA T	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1351	TTGCGATCAGTG ACATCACCTAGC G	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1352	TTGCAATCCCAA GACCGCAGAGCC C	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1353	TTGACCGCTAGG TGATGTCACTGA T	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1354	TTGAATCTTCTT GGTATGGGCTCT G	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1355	TTCTTGGTATGG GCTCTGCGGTCT T	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1356	TTCGGACTTGTT TCCTCTTTGGAA T	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1357	TTCCTCTTTGGA ATTGTTGCGATC A	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1358	TTCAAAGAGGA AACAAGTCCGAA G	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1359	TTATTGCTGTTG ATAATTGTGCAG T	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1360	TGTTTCCTCTTTG GAATTGTTGCGA	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1361	TGTTGCGATCAG TGACATCACCTA G	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1362	TGTCACTGATCG CAACAATTCCAA A	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1363	TGGTATGGGCTC TGCGGTCTTGGG A	TIC21	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1364	TTTGCTATGCAA CAAACCTTTCAAG A	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1365	TTTCAAGACTAT GATGAGCCAGAT G	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1366	TTGTTGCATAGC AAATTTCTTCAA C	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1367	TTGCTATGCAAC AACTTTCAAGA C	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1368	TTGCATAGCAAA TTTCTTCAACCA T	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1369	TTCAAGACTATG ATGAGCCAGATG G	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1370	TGTTGCATAGCA AATTTCTTCAAC C	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1371	TGGTTGAAGAAA TTTGCTATGCAA C	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1372	TGGCTCATCATA GTCTTGAAAGTT T	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1373	TGCTATGCAACA AACTTTCAAGAC T	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1374	TGCATAGCAAAT TTCTTCAACCAT G	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1375	TGCAACAACTT TCAAGACTATGA T	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1376	TGAAGAAATTTG CTATGCAACAAA C	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1377	TCTTGAAAGTTT GTTGCATAGCAA A	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1378	TCTGGCTCATCA TAGTCTTGAAAG T	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1379	TCCCATCTGGCT CATCATAGTCTT G	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1380	TCATCATAGTCT TGAAAGTTTGT G	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1381	TCATAGTCTTGA AAGTTTGTGCA T	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1382	TCAAGACTATGA TGAGCCAGATGG G	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1383	TATGCAACAAAC TTTCAAGACTAT G	TIC40	10	Amaranthus albus, Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1384	TTAAGTTGAATC AGCTCACATGGT C	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1385	TCTTCTCGGAAC ATATTCATGGCT T	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1386	TCTTAAGTTGAA TCAGCTCACATG G	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1387	TCATGTCCTTGA TTACAGCTTTAC T	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1388	TAAGTTGAATCA GCTCACATGGTC C	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1389	TAAAGCTGTAAT CAAGGACATGA GG	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1390	GTCTTAAGTTGA ATCAGCTCACAT G	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1391	GTAAAGCTGTAA TCAAGGACATGA G	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1392	GGACCATGTGAG CTGATTCAACTT A	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1393	GCCTCATGTCCT TGATTACAGCTT T	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1394	GCCATGAATATG TTCCGAGAAGAT G	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1395	GCATCTTCTCGG AACATATTCATG G	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1396	GAGGACCATGTG AGCTGATTCAAC T	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1397	GACCATGTGAGC TGATTCAACTTA A	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1398	CTTAAGTTGAAT CAGCTCACATGG T	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1399	CTCATGTCCTTG ATTACAGCTTTA C	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1400	CGCCTCATGTCC TTGATTACAGCT T	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1401	CCTCATGTCCTT GATTACAGCTTT A	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1402	CCATGTGAGCTG ATTCAACTTAAG A	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1403	CCATGAATATGT TCCGAGAAGATG C	TIC56	8	Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1404	TTGGTACTGGTA ATGATGCAGCAC C	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1405	TGGTGGTGCTGC ATCATTACCAGT A	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1406	TGGTGCTGCATC ATTACCAGTACC A	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1407	TGGTACTGGTAA TGATGCAGCACC A	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1408	TGGTAATGATGC AGCACCACCAGA T	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1409	TGCTGCATCATT ACCAGTACCAAT G	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1410	TGCAGCACCACC AGATTCTTCATC A	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1411	TGATGCAGCACC ACCAGATTCTTC A	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1412	TGATGAAGAATC TGGTGGTGCTGC A	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1413	TGAAGAATCTGG TGGTGGTGCTGCATC A	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1414	TCTGGTGGTGCT GCATCATTACCA G	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1415	TACTGGTAATGA TGCAGCACCACC A	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1416	TAATGATGCAGC ACCACCAGATTC T	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1417	GTGGTGCTGCAT CATTACCAGTAC C	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1418	GTGCTGCATCAT TACCAGTACCAA T	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1419	GTACTGGTAATG ATGCAGCACCAC C	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1420	GTAATGATGCAG CACCACCAGATT C	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1421	GGTGGTGCTGCA TCATTACCAGTA C	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1422	GGTGCTGCATCA TTACCAGTACCA A	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1423	GGTACTGGTAAT GATGCAGCACCA C	TOC132	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1424	TGGACACCCATG GTTGGGACCATG A	TOC159	10	Abutilon theophrasti, Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1425	TCATGGTCCCAA CCATGGGTGTCC A	TOC159	10	Abutilon theophrasti, Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1426	GGCTGGATTAC AGACAAGAGAT CT	TOC159	10	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1427	GACACCCATGGT TGGGACCATGAT T	TOC159	10	Abutilon theophrasti, Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Senna obtusifolia
1428	CAATCATGGTCC CAACCATGGGTG T	TOC159	10	Abutilon theophrasti, Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Senna obtusifolia
1429	AGATCTCTTGTC TGTGAATCCAGC C	TOC159	10	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Chenopodium album
1430	ACACCCATGGTT GGGACCATGATT G	TOC159	10	Abutilon theophrasti, Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Senna obtusifolia
1431	AATCATGGTCCC AACCATGGGTGT C	TOC159	10	Abutilon theophrasti, Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Senna obtusifolia
1432	TTTGTGGGACAG CGTAGTCATATT A	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1433	TTTGTTACCTG CACAGTTACTGC T	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1434	TTTGAGCGAGTA GCATAGCAACAA T	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1435	TTTCCTTGAACA TCCTGGTTCTTG G	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1436	TTTCCTCCGATT GCCAAGTCTCCT C	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1437	TTTCCCAAGAAC CAGGATGTTCAA G	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1438	TTTATGTGGATA GGCTGGATTAC A	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1439	TTTACCTTCTCTT CACCAAATATTG	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1440	TTGTGGGACAGC GTAGTCATATTA T	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1441	TTGTCTGTGAAT CCAGCCTATCCA C	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1442	TTGTCCTCAAGA TGGGTAGATCAT T	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1443	TTGGTTACCTGC ACAGTTACTGCT G	TOC159	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1444	TTTGGTCAAGAC TATCATTGATGT T	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1445	TTTCTTCTGGAT AAGACAATCGAT G	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1446	TTTCATGGATAC CAAATTTGGTCA A	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1447	TTGTCTTATCCA GAAGAAAGCCTT T	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1448	TTGTCAACCAAG ATACCCTTACTT C	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1449	TTGGTCAAGACT ATCATTGATGTT G	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1450	TTGACCAAATTT GGTATCCATGAA A	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1451	TTCTTCTGGATA AGACAATCGATG T	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1452	TTCTGGATAAGA CAATCGATGTAT T	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1453	TTCATGGATACC AAATTTGGTCAA G	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1454	TGTCAACCAAGA TACCCTTACTTC C	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

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SEQ ID NO	Seq	Gene	# Species	Species
1455	TGGTCAAGACTA TCATTGATGTTG T	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1456	TGGATACCAAAT TTGGTCAAGACT A	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1457	TGGATAAGACAA TCGATGTATTGC T	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1458	TGGAAGTAAGG GTATCTTGTTG AC	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1459	TGATGGATTGAG TTACGAAGACTT C	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1460	TGATAGTCTTGA CCAAATTTGGTA T	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1461	TGACCAAATTTG GTATCCATGAAA C	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1462	TCTTGACCAAAT TTGGTATCCATG A	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1463	TCTTCTGGATAA GACAATCGATGT A	TOC34	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1464	TACAGGAGAATG GGCAAGGGTTCG T	TOC75	10	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Euphorbia heterophylla
1465	GACGAACCCTTG CCCATTCTCCTG T	TOC75	10	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Euphorbia heterophylla

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SEQ ID NO	Seq	Gene	# Species	Species
1466	ACGAACCCTTGC CCATTCTCCTGT A	TOC75	10	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Euphorbia heterophylla
1467	ACAGGAGAATG GGCAAGGGTTTCG TC	TOC75	10	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis, Euphorbia heterophylla
1468	TTTGCTGAACAT GGAAACGATCTT G	TOC75	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1469	TTTGAAATGGTT TCTTTGAGACCT G	TOC75	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1470	TTTCTTCAATGG TGGAAACGGAG GT	TOC75	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1471	TTTCTCAAAGCT TGCTTGCTGCT T	TOC75	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1472	TTTCAGTCATAT CAGGATCCATCT C	TOC75	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1473	TTTCAAAGAATG AATCTTCAGTAC C	TOC75	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1474	TTTATATTTCTCA AAGCTTGCTTGC	TOC75	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1475	TTTAGTTACTTG TGGAATGTTTGA G	TOC75	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1476	TTTACAGGAGAA TGGGCAAGGGTT C	TOC75	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

(continued)

SEQ ID NO	Seq	Gene	# Species	Species
1477	TTTAATATAGAA GCAGGCAAGCA AG	TOC75	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1478	TTGTGTGGGAGA CCTTCCAAGTTA T	TOC75	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1479	TTGGTGCAGCTA GAAACATTCTTG A	TOC75	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1480	TTGGTACTGAAG ATTCATTCTTTG A	TOC75	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1481	TTGCTTGCCTGC TTCTATATTA G	TOC75	9	Amaranthus albus, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1482	TTGCTGAACATG GAAACGATCTTG G	TOC75	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis
1483	TTGCCATTCTC CTGTAAACTTCA G	TOC75	9	Amaranthus chlorostachys, Amaranthus graecizans, Amaranthus hybridus, Amaranthus lividus, Amaranthus palmeri, Amaranthus rudis, Amaranthus spinosus, Amaranthus thunbergii, Amaranthus viridis

Example 3. Enhanced plant sensitivity to glyphosate.

[0059] In this example, growing *Amaranthus palmeri* are treated with a topically applied composition for inducing modulation of a target gene in a plant including (a) an agent for conditioning of a plant to permeation by polynucleotides and (b) polynucleotides including at least one polynucleotide strand including at least one segment of 19-25 contiguous nucleotides or more of the target gene of SEQ ID NO: 1-1263 or SEQ ID NO: 1584-1638. Target genes associated with the chloroplast protein import system include but are not limited to the structural genes that encode for translocon outer membrane (Toc) complex proteins, translocon inner membrane complex proteins (Tic), stroma processing peptidase, and chaperone like proteins.

[0060] The following procedure is used for all assays described in this example. Approximately four-week old *Amaranthus palmeri* plants (glyphosate-resistant Palmer amaranth, "R-22") are used in this assay. Plants are treated with 0.5-1.0 percent Silwet L-77 solution freshly made with ddH₂O. Two fully expanded leaves per plant (one cotyledon, one true leaf) are treated with the polynucleotide/Silwet L-77 solution. Final concentration for each dsRNA polynucleotide was 25 microM) unless otherwise stated. Twenty microliters of the solution are applied to the top surface of each of the two pre-treated leaves to provide a total of 40 microliters (1-4 nmol polynucleotide) for each plant.

[0061] Spray solutions are prepared the same day as spraying. Single oligonucleotide molecules are applied at rates between 0.04 and 0.18 mg/ml in 20mM potassium phosphate buffer (pH 6.8) are added to spray solutions 15 to 50 minutes before spraying. One-to-two-ml spray solutions were applied using a custom low-dead-volume sprayer ("milli applicator") at 8-30 gpa (gallons per acre) to one-to-four inch tall plants. Treated plants are place in a greenhouse set

for either a 26.7/21.1°C or 29.4/21.1°C 14/10 hour temperature and supplemental light schedule. The amount of response relative to unsprayed treatments is collected at various time intervals up to 21 days after treatment.

[0062] A common spray nozzle used for all applications made with the track sprayer is the Turbo Teejet air induction nozzle (015) nozzle with air pressure set at a minimum of 20 psi (pounds per square inch or 160kpa). This style nozzle is currently being utilized to lessen shear forces that can damage or otherwise change large macromolecules that can be seen with other nozzle styles. The height of the spray nozzle is to be 16-18 inches above top of plant material. Treatments are to be made when plants reach the desired size, height or leaf stage.

[0063] Application rates are chosen so as to achieve percent control ratings in the range of 50 percent at the lowest rate to 90 percent control at the highest rate. The rates in this control range provide the best possible efficacy comparisons among formulations, allowing separation of relative performance of test samples. The rate of herbicide used in these studies is typically at the manufacturer's recommended use rate. On occasion lower or higher rates may be necessary depending on test objectives. The rate structure used for a given test will be dependent on the environmental conditions at the time of spray application (time of year), the plant species being treated (highly susceptible or tough to kill) and age (or size) of plants to be treated.

[0064] When various Toc75 trigger dsRNA polynucleotides (Table 3, SEQ ID NO: 1484-1534) were applied to a glyphosate resistant *A. palmeri* biotype (R22) followed by (fb) treatment with glyphosate herbicide (WeatherMax®, Monsanto Co., St Louis, herein referred to as WMAX), the results shown in Table 4 show the percent of treated plants demonstrating a reduction in growth. The controls are: untreated (no formulation, no polynucleotide), untreated fb 2X WMAX, formulation (polynucleotide/Silwet L-77 solution) fb 2X WMAX, the EPSPS (5-enolpyruvylshikimate-3-phosphate synthase) target oligo positive control were four polynucleotides (1, 3, 4, 5 at 4nm/plant) that target the *A. palmeri* EPSPS coding sequence. The treatments are pools of Toc75 fb 2X WMAX polynucleotides with the formulation. The plants were scored 7, 14, and 21 days after treatment (DAT). The experimental results shown in Table 4, demonstrated that the treated glyphosate resistant plants become more sensitive to the herbicidal effect of glyphosate when the treatment included polynucleotides homologous or complementary to a chloroplast protein import system gene of the plant.

Table 3. Toc75 polynucleotides

Oligo	SEQ ID NO:	Polynucleotide sequence
52	1484	CTTCTTGCCTGCTTCAATGTTATA
53	1485	CCCAGAGAGGTTATATTTCTCAAAG
54	1486	ATGGACTTCAATGTTTGAAAATAAT
55	1487	CTTCATTCTGTTCATCATGCCGAGT
55	1488	CTTCATTCTGTTCATCATGCCGAGT
56	1489	AGCTTAATCTCAACAATAATTCCTC
56	1490	AGCTTAATCTCAACAATAATTCCTC
57	1491	CAATATTCCACTCTGTAGTTAGTTC
58	1492	CAATATTCCACTCTGTAGTTAGTTC
59	1493	TTTGGACGACCATGAGGCCAGGAA
60	1494	CCCACCTGGCTGTAAAGAAGCCAGT
61	1495	TGTTTCGGTGTTGAAAAGAGACGGT
62	1496	TGTAATGATCTATTAAGACCTTTGA
63	1497	GTAGTTATCAGTGGTTACTGAACCA
64	1498	ATGCAAGATCGTCCTTTGGATTAAG
65	1499	TACGGA TGCACA TATCAAACCTTGA
66	1500	GCTAGGATTATATACACCATCAATA
67	1501	AGCAGCTTGCTTTGAAAGTTCGGTT
68	1502	ACAGGACTCAGCTTTCTGCTATTGA
69	1503	ATCCAGTCCTGGGCCACCGGTAAAC
70	1504	TATCAACCCAAATAGGAGGAACTTC

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Oligo	SEQ ID NO:	Polynucleotide sequence
71	1505	GTAATATTTGCTTTCAGACCAGATC
72	1506	CTTACTCTGCCTTGTGTAATTCTCG
73	1507	CTTCACATACAAGCCCATAAGTAAA
74	1508	CTGCTTTCATCCCGTGTGTAATCT
75	1509	CCTCTGGCCAGTAGTGGCAATATGG
76	1510	CACTAATTCCACCATTTGGCAAAAT
77	1511	CTTAAAGTTGTTGGAGGCCCATCAG
78	1512	CACCATACGATCAACACCAGTACCA
79	1513	CTCTTGTAATATTTGCCTGTGCGAA
80	1514	GCACCA TTT ACAAACTTTGT ATT AT
81	1515	AAACACA TTTCTGTCACCAACT AT A
82	1516	CTATCCCAAGGCCTTGGTCTACCTG
83	1517	CGGTTGAAAATTGGGAATTTAGTGC
84	1518	GAAGTTGGTTAGTGTGAGTTGATGA
85	1519	CTTCTTCAACTTCCGTCAGTTGGAG
86	1520	ACTGGTGGTGGTGAATTTCCAGCAC
87	1521	AGCATAGTGACCATGTAGGACAAGA
88	1522	AACTTGGAAGGTCTCCACACAACC
89	1523	GGTCCCCCAAGGGTGAAAGCCTCAT
90	1524	CATGTTGTAACCCCTAACTGAATAG
91	1525	TGTTTCTAGCTGCACCAAGTTCCCC
92	1526	CGTAACTCAGCAGCAAGCTCAAGAA
93	1527	CACATGTGTGGTCTTGACAGGTATC
94	1528	CGTTTCCATGTTTACGCAAACGCATA
95	1529	TTCACGTCTTTAGAGGTTCCAAGAT
96	1530	CCTGTAACTTCAAGTGGGATTACCC
97	1531	CATAAGACGAACCCCTGCCCATTCT
98	1532	ACAAGACCAAGCTTGACACCAACTC
99	1533	ATGATCGACAGCATACTCGGCTCGA
100	1534	AAAATAATGAGCCGGTACCAGAATT

Table 4. *A. palmeri* plants treated with TOC75 trigger polynucleotides and glyphosate show enhanced sensitivity to glyphosate, percent growth reduction 7, 14, and 21 DAT

Plant	Polynucleotide treatment	herbicide	Days after treatment		
			7	14	21
R22	Untreated control	no	0	0	0
R22	Untreated control	no	0	0	0
R22	Untreated control fb 2X WMAX	2X Weather MAX	0	30	25

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(continued)

	Plant	Polynucleotide treatment	herbicide	Days after treatment		
				7	14	21
5	R22	Untreated control fb 2X WMAX	2X Weather MAX	0	30	25
	R22	Untreated control fb 2X WMAX	2X Weather MAX	0	20	0
	R22	Untreated control fb 2X WMAX	2X Weather MAX	0	20	0
10	R22	Formulation control fb 2X WMAX	2X Weather MAX	25	50	40
	R22	Formulation control fb 2X WMAX	2X Weather MAX	25	50	30
	R22	Formulation control fb 2X WMAX	2X Weather MAX	25	50	40
15	R22	Formulation control fb 2X WMAX	2X WeatherMAX	25	40	30
	R22	EPSPS target (oligo 1, 3, 4, 5 @4nm/ plant)	2X Weather MAX	75	80	80
	R22	EPSPS target (oligo 1, 3, 4, 5 @4nm/ plant)	2X Weather MAX	85	90	90
20	R22	EPSPS target (oligo 1, 3, 4, 5 @4nm/ plant)	2X Weather MAX	75	90	90
	R22	EPSPS target (oligo 1, 3, 4, 5 @4nm/ plant)	2X Weather MAX	85	90	90
25	R22	TOC75 Set 1 (oligo 52, 53, 54, 55, 56 @ 4nm/plant)	2X Weather MAX	50	60	45
	R22	TOC75 Set 1 (oligo 52, 53, 54, 55, 56 @ 4nm/plant)	2X Weather MAX	85	85	70
30	R22	TOC75 Set 1 (oligo 52, 53, 54, 55, 56 @ 4nm/plant)	2X Weather MAX	85	85	70
	R22	TOC75 Set 1 (oligo 52, 53, 54, 55, 56 @ 4nm/plant)	2X Weather MAX	75	80	60
35	R22	TOC75 Set 2 (oligo 57, 58, 59, 60, 61 @ 4nm/plant)	2X Weather MAX	65	80	70
	R22	TOC75 Set 2 (oligo 57, 58, 59, 60, 61 @ 4nm/plant)	2X Weather MAX	75	80	60
40	R22	TOC75 Set 2 (oligo 57, 58, 59, 60, 61 @ 4nm/plant)	2X Weather MAX	75	80	75
	R22	TOC75 Set 2 (oligo 57, 58, 59, 60, 61 @ 4nm/plant)	2X Weather MAX	75	70	60
45	R22	TOC75 Set 3 (oligo 62, 63, 64, 65, 66 @ 4nm/plant)	2X Weather MAX	50	50	60
	R22	TOC75 Set 3 (oligo 62, 63, 64, 65, 66 @ 4nm/plant)	2X Weather MAX	25	50	60
50	R22	TOC75 Set 3 (oligo 62, 63, 64, 65, 66 @ 4nm/plant)	2X Weather MAX	25	50	40
	R22	TOC75 Set 3 (oligo 62, 63, 64, 65, 66 @ 4nm/plant)	2X Weather MAX	25	40	40
55	R22	TOC75 Set 4 (oligo 67, 68, 69, 70, 71 @ 4nm/plant)	2X Weather MAX	10	30	30

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(continued)

	Plant	Polynucleotide treatment	herbicide	Days after treatment		
				7	14	21
5	R22	TOC75 Set 4 (oligo 67, 68, 69, 70, 71 @ 4nm/plant)	2X Weather MAX	25	40	30
	R22	TOC75 Set 4 (oligo 67, 68, 69, 70, 71 @ 4nm/plant)	2X Weather MAX	40	60	50
10	R22	TOC75 Set 4 (oligo 67, 68, 69, 70, 71 @ 4nm/plant)	2X Weather MAX	25	40	25
	R22	TOC75 Set 5 (oligo 72, 73, 74, 75, 76 @ 4nm/plant)	2X Weather MAX	25	50	40
15	R22	TOC75 Set 5 (oligo 72, 73, 74, 75, 76 @ 4nm/plant)	2X Weather MAX	25	50	50
	R22	TOC75 Set 5 (oligo 72, 73, 74, 75, 76 @ 4nm/plant)	2X Weather MAX	25	50	50
20	R22	TOC75 Set 5 (oligo 72, 73, 74, 75, 76 @ 4nm/plant)	2X Weather MAX	25	30	25
	R22	TOC75 Set 6 (oligo 77, 78, 79, 80, 81 @ 4nm/plant)	2X WeatherMAX	35	50	25
25	R22	TOC75 Set 6 (oligo 77, 78, 79, 80, 81 @ 4nm/plant)	2X Weather MAX	25	50	30
	R22	TOC75 Set 6 (oligo 77, 78, 79, 80, 81 @ 4nm/plant)	2X Weather MAX	35	50	30
30	R22	TOC75 Set 6 (oligo 77, 78, 79, 80, 81 @ 4nm/plant)	2X Weather MAX	50	60	50
	R22	TOC75 Set 7 (oligo 82, 83, 84, 85, 86 @ 4nm/plant)	2X Weather MAX	25	30	30
35	R22	TOC75 Set 7 (oligo 82, 83, 84, 85, 86 @ 4nm/plant)	2X Weather MAX	0	10	30
	R22	TOC75 Set 7 (oligo 82, 83, 84, 85, 86 @ 4nm/plant)	2X Weather MAX	35	40	30
40	R22	TOC75 Set 7 (oligo 82, 83, 84, 85, 86 @ 4nm/plant)	2X Weather MAX	10	30	20
	R22	TOC75 Set 8 (oligo 87, 88, 89, 90, 91 @ 4nm/plant)	2X Weather MAX	25	30	25
45	R22	TOC75 Set 8 (oligo 87, 88, 89, 90, 91 @ 4nm/plant)	2X Weather MAX	25	20	25
	R22	TOC75 Set 8 (oligo 87, 88, 89, 90, 91 @ 4nm/plant)	2X Weather MAX	25	50	40
50	R22	TOC75 Set 8 (oligo 87, 88, 89, 90, 91 @ 4nm/plant)	2X Weather MAX	35	50	40
	R22	TOC75 Set 9 (oligo 92, 93, 94, 95, 96 @ 4nm/plant)	2X Weather MAX	50	60	40
55	R22	TOC75 Set 9 (oligo 92, 93, 94, 95, 96 @ 4nm/plant)	2X Weather MAX	50	60	50

(continued)

Plant	Polynucleotide treatment	herbicide	Days after treatment		
			7	14	21
R22	TOC75 Set 9 (oligo 92, 93, 94, 95, 96 @ 4nm/plant)	2X Weather MAX	75	80	60
R22	TOC75 Set 9 (oligo 92, 93, 94, 95, 96 @ 4nm/plant)	2X Weather MAX	75	65	50
R22	TOC75 Set 10 (oligo 97, 98, 99, 100 @ 4nm/plant)	2X Weather MAX	60	65	65
R22	TOC75 Set 10 (oligo 97, 98, 99, 100 @ 4nm/plant)	2X Weather MAX	60	70	70
R22	TOC75 Set 10 (oligo 97, 98, 99, 100 @ 4nm/plant)	2X Weather MAX	60	75	70
R22	TOC75 Set 10 (oligo 97, 98, 99, 100 @ 4nm/plant)	2X Weather MAX	65	80	70

Example 4. OEP80 gene and Stroma processing peptidase gene target results.

[0065] *Amaranthus palmeri* plants (R22 glyphosate resistant biotype) were treated following the protocol described in Example 3. Trigger dsRNA polynucleotides shown in Table 5 (SEQ ID NO: 1535-1573, plus strand sequence illustrated) are targeting the *A. palmeri* OEP80 gene coding region (SEQ ID NO: 365). The polynucleotides were topically applied at 8 nmol/plant in a composition comprising 0.5-1.0 percent Silwet L-77 and buffer followed one day later by treatment with 2X WeatherMAX (WMAX). Injury rating of the treated plants was conducted 14 days after the WMAX treatment. The control treatments were buffer alone and 2 rates (4 nmol and 8 nmol) of a trigger polynucleotide (oligo 5.3) targeting the *A. palmeri* EPSPS coding gene sequence. The average baseline level of injury effect of buffer plus WMAX was set at 40 percent for this experiment. The results illustrated in Figure 1 demonstrated that at least 18 polynucleotides (T25452, T25454, T25455, T25456, T25457, T29847, T29848, T25464, T25465, T25466, T25471, T25472, T25473, T25474, T25475, T25477, T25478 and T29213) were able to enhance the effect of WMAX on this glyphosate resistant biotype. Additionally, 4 regions of the target gene sequence were identified in which the polynucleotides in those regions were particularly effective, these regions are between nucleotide positions 369-701, 1016-1168, 1364-1622 and 1683-1792 of SEQ ID NO: 365.

Table 5. Polynucleotide trigger molecules for *A. palmeri* OEP80

SEQ ID NO	Oligo test ID	Polynucleotide sequence
1535	T25445	GTTATCCCTGAGTCGACCCACTAACTCAACTCAGTCCAAAAAC CCTTCAATTTC
1536	T25446	GTCCAAAAACCCTTCAATTTCCTTCTGTCAATCCCTAAATTCTA CTCTC
1537	T25447	GTCAATCCCTAAATTCTACTCTCTTACAAGCCAAATTCTCAATT ACCCAGTTCATTAATGGC
1538	T25448	GCATCAAACCTCCACGGAAACCCCGTTAAGTTTCAATCTTCTCC ATCACCATTGC
1539	T25449	GCTATGCTCTTCAACATTGTCTTTGAACGACTCAACTCAGCCTC CAGC
1540	T25450	GCCGGAAGTGGTAGTGTGGTTGAGGTTAGTCAATCGAAATCG GCTTCAGTGAGTCGTAC

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(continued)

SEQ ID NO	Oligo test ID	Polynucleotide sequence
5	1541	T25451 GTACTCGAAGGGAGGATGAAGAGAGAGTGTGATTAGTGAGG TGTTAGTGAGGAGTAAAGATGGAGAAGAATTAGAGAGGAAAG ATTTGGAATC
10	1542	T25452 GGAGGCATTAATGGCATTGAAAGCTTGCCGGGCGAATTCAGC TTTGA CTGTGC
15	1543	T25453 GAGAGGTTTCAGGAGGATGTTACAGAATTATTGATAGTGGGT ATTTTTCTTCATGTATGCCAGTTGCAGTGGATAC
20	1544	T25454 GATACTAGGGATGGTATTAGATTGGTCTTTCAGGTAGAACCAA ACCAGGAGTTTAGAGGACTGGTGTGC
25	1545	T25455 GCGAAGGAGCTAATGTTCTCCCTTCCAAGTTTGTAGAGGATTC ATTTC
30	1546	T25456 GTGATGGATATGGGAAAGTGGTCAATATCAGGCGTTTGGATG AAGTGATTGATTC
35	1547	T25457 GATTCTATAAATGGATGGTACATGGAGCGTGGTCTTTTTGGCA TGGTTTC
40	1548	T25458 GTTTCTGGTGTGAGATACTTTCAGGGGGTATACTAAGGTTAC AAATTTCTGAAGC
45	1549	T25459 GCTGAGGTCAATGATGTTTCAATCCGCTTCCTTGATCGTAAGA CACGTGAGCCAAC
50	1550	T25460 GCCAACTGTTGGGAAGACAAAGCCAGAAACAATACTTCGACA ACTTACAACAAAAAAGGAC
55	1551	T25461 GACAGGTATACAGTTTGAATCAAGGGAAAAGGGATGTTGAGA CTGTTTTGAC
	1552	T25462 GACGATGGGAATCATGGAAGATGTAAGCATTTTTCCCCAGCCT GCTGGAGATAC
	1553	T25463 GATACAGGTAAAGTTGATTTGGTAATGAATGTGGTTGAGCGTG TGAGTGGTGGTTTC
	1554	T25464 GTTTCTCGGCTGGTGGTGGTATTTTCGAGCGGGATAACGAGCGG ACCGC
	1555	T25465 GCTATCAGGTTTAATTGGAAGCTTTCATATTCTCACAGGAAT CTGTTTGGAAAAAATC
	1556	T25466 GAAAAAATCAAAAAGTAAATGTCTCTCTTGAAAGAGGCCAAA TCGACTCTATCTTCC
	1557	T25467 GGATAAATTATACAGTCCCATGGATTGAAGGTGATGATAAGC GTACTCAAAGGTC

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(continued)

SEQ ID NO	Oligo test ID	Polynucleotide sequence
1558	T25468	GTCAATCATTATTCAGAACTCAAGGACTCCGGGTACTTTGGTC CATGGTAATC
1559	T25469	GTAATCAACCTGAAAATAGTAACTTAACTATTGGCCGTGTAAC AGCTGGC
1560	T25470	GCATCGAATTCAGCCGGCCCCCTAAGACCCAAATGGAGCGGAA CAGCTGGAC
1561	T25471	GACTTACGTTTCAGCATGCTGGTGTCCGTGATGAAAAAGGGAA CCCCGTC
1562	T25472	GTCATAAAAGATTTCTACAACAGCGCTCTTACGGCAAGTGGGA ATACTCATGATAATATGC
1563	T25473	GCTGCTTGCCAAAGGCGAGTGTGCCTACACGGGTGACTTAGG ATCCTCAATGTTAGTC
1564	T25474	GTCTTAAGCATGGAACAAGGTCTTCCTATCTATCCTGAGTGGC TGTGTTTTAATC
1565	T25475	GTTTTAATCGAGTCAACGCTCGTGCTAGGTCAGGGGTGGACAT TGGTCCAGC
1566	T25476	GCTAATCTTTTTCTCAGTTTGTCTGGTGGTCATGTGGTCGGTAA ATTTCCTCCTCATGAAGC
1567	T25477	GTTTGCGATCGGTGGTACAAATAGTGTGAGAGGATATGAAGA AGGTGCCGTTGGC
1568	T25478	GCTCAGGCCTTTCATACGTAGTGGGCTGTGGAGAAGTTTCCTT CCCTCTGTATGGTC
1569	T25479	GTCCAGTAGATGGCGCTCTTTTTGCTGATTATGGAACGGATCT CGGATCAGGTTC
1570	T25480	GTTCATTGGTTCCTGGTGATCCTGCTGGTGCGAGATTAACC CGGGAGTGGATAC
1571	T25481	GGCTATGGATTTGGTATCCGTGTCGAGTCTCCATTAGGTCCTCT ACGGTTAGAGTATGC
1572	T25482	GCATTTAACGACAGACAAGCGAGGCGGTTTCATTTTGGCGTAG GTCATCGGAAC
1573	T29213	GGATATGAAGAAGGTGCCGTTGGC

[0066] Stroma processing peptidase is a key enzyme in the chloroplast protein import system of plants. *Amaranthus palmeri* plants (R22 glyphosate resistant biotype) were treated following the protocol described in Example 3. Trigger dsRNA polynucleotides shown in Table 6 (SEQ ID NO: 1574-1583, plus strand sequence illustrated) are targeting the *A. palmeri* stroma processing peptidase (SPP, SEQ ID NO: 936) or Toc75 gene coding region (SEQ ID NO: 260). The SPP polynucleotides were topically applied in 2 pools of polynucleotides, oligos 1, 4, 5, and 6, and oligos 2, 7, 8, and 9, at 3nmol each/plant in a composition comprising 0.1 percent Silwet L-77 and buffer followed one day later by treatment

with 2X WeatherMAX (WMAX). Injury rating of the treated plants was conducted 21 days after the WMAX treatment. The control treatments were buffer alone and a pool of 4 nmol each of 4 trigger polynucleotides (oligo 1, 2, 3, and 5) targeting the *A. palmeri* EPSPS coding gene sequence. The average baseline level of injury effect of WMAX treatment was 41 percent for this experiment. The results shown in Table 7 demonstrate that targeting the stroma processing peptidase gene with trigger polynucleotides homologous or complementary to the gene coding sequence enhanced the sensitivity of the plants to the herbicidal effects of glyphosate.

Table 6. Sequence of trigger molecules for Toc75 and stroma processing peptidase gene targets

Oli go no.	SEQ ID NO	Sequence	Gene target
1	1574	TCAAGAAGTGGGATGTTGATAAAAAATAAAAAATTTTCATGA	SPP
2	1575	TGAAAGGTGTTCTAGAGGATGACATTCAAAAAGTCGAAGA	SPP
3	1576	GCAaGAAAGCTTTGAGAAaTATAACCTCTcTGGGATtATT	TOC75
4	1577	CGGAGAAGAGGGTCATTAATAAAAAATGTTTCGTTCAAGAT	SPP
5	1578	ATTTAGTCAGACTGGCTTGGAGAATGAGACAGAGGCTTCCC	SPP
6	1579	ATTAAAGACACTGATGAAAGAGCCTGTGCCTATATTGCTGG	SPP
7	1580	AGAAATATCCCGCTGGTGATGGCGGTGATTTAAAGAAAAAG	SPP
8	1581	TGACATGAGTTTCTTGAAGCAAGAGCTACTTTCATTAGTA	SPP
9	1582	CTGTGGCATCTCCAGAAGACGTCGAAGCTGTAAAGAAAAT	SPP
10	1583	TCTTGAGCTTGCTGCTGAGTTACGGATACCTGTCAAGACCA	TOC75

Table 7. Stroma processing peptidase and Toc75 results

Treatment	replications	Percent control 14 DAT	Stdev
Buffer alone	4	0	0
EPSPS target (oligo 1, 3, 4, 5 @4nm/plant)	4	97	4
Stroma Processing Peptidase 1 (oligo 1, 4, 5, 6 @ 3nm/plant)	4	64	6
Stroma Processing Peptidase 2 (oligo 2, 7, 8, 9 @ 3nm/plant)	4	65	17
TOC75 (oligo 3, 10 @ 3nm/plant)	4	83	12
Buffer + glyphosate	4	41	15

Example 5. Enhanced herbicide resistant plant sensitivity to glyphosate.

[0067] In this example, herbicide resistant *Amaranthus palmeri* (R-22) plants were treated with a topically applied composition comprising a dsRNA molecule comprising an antisense strand polynucleotide sequence identified as SEQ ID NO: 1639 (GAUUACCCUUGACGUCUUUAGAGCUUCCAAGAUCGUUCCAUGUUCAGC) or a dsRNA molecule comprising the antisense strand polynucleotide sequence identified as SEQ ID NO: 1640 (GACCCUUGAUGUUUCUGUGUUCAAAAGAGACAGUUCGCCUGGCUGGAAGGA AGC) for inducing modulation of expression of a target TOC75 gene in the *Amaranthus* plant including an agent for conditioning of a plant to permeation by dsRNA polynucleotides.

[0068] Approximately four-week old *Amaranthus palmeri* plants (glyphosate-resistant Palmer amaranth, "R-22") propagated from cutting were used in this assay. Plants were treated with a formulation composition of 0.5 percent Silwet L-77, 20 mM sodium phosphate buffer, 2 percent ammonium sulfate with or without the dsRNA polynucleotides (SEQ ID NO: 1639 or SEQ ID NO: 1640). The amount of dsRNA polynucleotide applied to each plant in the treatments was 2, 4, 8 and 16 nmol. Four replications of each treatment were conducted. The treatment with the TOC75 trigger dsRNA polynucleotides (SEQ ID NO: 1639 or SEQ ID NO: 1640) at various nanomole (nmol) doses was followed by (fb) treatment with a glyphosate herbicide (WeatherMax®, Monsanto Co., St Louis, herein referred to as WMAX) 24 hours after the formulation treatment. 2X WMAX is equal to 2058 grams active ingredient/hectare (g ai/ha). The results in Table 8 show the mean percent of treated plants demonstrating a reduction in growth measured as plant height relative to untreated control plants (no formulation or WMAX applied). The formulation control is without the polynucleotides and fb 2X WMAX.

All treatments of the formulation containing the dsRNA polynucleotides are fb 2X WMAX. The plants were scored 11 days after treatment (DAT). The experimental results, demonstrated that the treated herbicide resistant plants became more sensitive to the herbicidal effect of glyphosate when the treatment included the dsRNA polynucleotides of SEQ ID NO: 1639 at a dose as low as 2 nmol or SEQ ID NO: 1640 at a dose as low as 8 nmol.

Table 8. Glyphosate resistant *A. palmeri* plants treated with TOC75 trigger polynucleotides and glyphosate show enhanced sensitivity to glyphosate, percent growth reduction 11 DAT

Treatments	Mean percent growth reduction of 4 replications	Standard deviation
Formulation control fb 2X WMAX	28	13
Formulation + dsRNA SEQ ID NO:1639 2nmol fb 2X WMAX	96	3
Formulation + dsRNA SEQ ID NO:1639 4nmol fb 2X WMAX	93	5
Formulation + dsRNA SEQ ID NO:1639 8nmol fb 2X WMAX	91	3
Formulation + dsRNA SEQ ID NO:1639 16nmol fb 2X WMAX	97	3
Formulation + dsRNA SEQ ID NO:1640 2nmol fb 2X WMAX	18	19
Formulation + dsRNA SEQ ID NO: 1640 4nmol fb 2X WMAX	29	10
Formulation + dsRNA SEQ ID NO: 1640 8nmol fb 2X WMAX	52	27
Formulation + dsRNA SEQ ID NO: 1640 16nmol fb 2X WMAX	99	0

Example 6. Enhanced herbicide resistant plant sensitivity to glyphosate (WMAX) or mesotrione (Callisto).

[0069] In this example, glyphosate resistant *Amaranthus palmeri* (R-22 or BL65, glyphosate resistant field isolated variants) plants were treated with a topically applied composition comprising a dsRNA molecule comprising an antisense strand polynucleotide sequence identified as SEQ ID NO: 1641 for inducing modulation of expression of a target OEP80 gene in the *Amaranthus* plant including an agent for conditioning of a plant to permeation by dsRNA polynucleotides. Approximately four-week old *Amaranthus palmeri* plants (glyphosate resistant R-22 or BL65) propagated from cutting were used in this assay. Plants were treated with a formulation composition of 0.5 percent Silwet L-77, 20 mM sodium phosphate buffer, 2 percent ammonium sulfate with or without the dsRNA polynucleotides (SEQ ID NO: 1641). The amount of dsRNA polynucleotide applied to each plant in the treatments was 16 nmol. Four replications of each treatment were conducted. The treatment with the OEP80 trigger dsRNA polynucleotides comprising an antisense polynucleotide (SEQ ID NO: 1641, 5'-GAAACCAUGCCAAAAAGACCACGCUCCAUGUACCAUCCAUUUUAUAGAAUC-3') and its complementary sense polynucleotide SEQ ID NO: 1547, also referred to as T25457) at 16 nmol was followed by (fb) treatment with a glyphosate herbicide (WeatherMax®, Monsanto Co., St Louis, herein referred to as WMAX) or mesotrione (Callisto®, Syngenta, Greensboro, NC) 24 hours after the formulation treatment. 2X WMAX is equal to 2058 grams active ingredient/hectare (g ai/ha) and 0.05X and 0.125X Callisto are equal to 5.2 and 13 grams active ingredient/hectare (g ai/ha), respectively. All treatments of the formulation containing the dsRNA polynucleotides are fb 2X WMAX or 0.05X Callisto or 0.125X Callisto. The plants were scored 14 days after treatment (DAT). The experimental results shown in Tables 9-12 demonstrated that the treated herbicide resistant plants became more sensitive to the herbicidal effect of glyphosate or Callisto® when the treatment included the dsRNA polynucleotides of T25457 at a dose of 16 nmol or T43701 (a dsRNA polynucleotide having a 2 nucleotide overhang at each 3' end consisting of nucleotide position 8-28 of SEQ ID NO: 1641 (underlined segment above) and nucleotide position 25-45 of SEQ ID NO: 1547) at a dose at a dose of 16 nmol.

[0070] The results in Table 9 and 10 show the results of two experiments that include the dsRNA polynucleotides (T25457 or T43701) which increased the mean percent of glyphosate treated plants demonstrating a reduction in growth measured as plant fresh weight relative to control plants (formulation fb 2X WMAX without the dsRNA molecules).

Table 9. Glyphosate resistant *A. palmeri* (BL65) plants treated with OEP80 trigger polynucleotides and glyphosate show enhanced sensitivity to glyphosate, percent growth reduction 14 DAT

Treatments	Mean percent growth reduction of 4 replications	Standard deviation
Formulaton control fb 2X WMAX	49	19
Formulation + dsRNA T25457 16nmol fb 2X WMAX	97	3

Table 10. Glyphosate resistant *A. palmeri* (R22) plants treated with OEP80 trigger polynucleotides and glyphosate show enhanced sensitivity to glyphosate, percent growth reduction 14 DAT

Treatments	Mean percent growth reduction of 4 replications	Standard deviation
Formulaton control fb 2X WMAX	16	15
Formulation + dsRNA T25457 16nmol fb 2X WMAX	86	8
Formulation + dsRNA T43701 16nmol fb 2X WMAX	85	13

[0071] The results in Table 11 and 12 show the results of two experiments that include the dsRNA polynucleotides (T25457 or T43701) which increased the mean percent of Callisto® treated plants demonstrating a reduction in growth measured as plant fresh weight relative to untreated control plants (formulation fb Callisto® without the dsRNA polynucleotides).

Table 11. Glyphosate resistant *A. palmeri* (BL65) plants treated with OEP80 trigger polynucleotides and callisto show enhanced sensitivity to Callisto®, percent growth reduction 14 DAT

Treatments	Mean percent growth reduction of 4 replications	Standard deviation
Formulaton control fb 0.125X Callisto®	30	17
Formulation + dsRNA T25457 16nmol fb 0.125X Callisto®	91	5

Table 12. Glyphosate resistant *A. palmeri* (R22) plants treated with OEP80 trigger polynucleotides and Callisto® show enhanced sensitivity to Callisto®, percent growth reduction 14 DAT

Treatments	Mean percent growth reduction of 4 replications	Standard deviation
Formulaton control fb 0.125X Callisto®	23	17
Formulation + dsRNA T25457 16nmol fb 0.125X Callisto®	65	5
Formulaton control fb 0.05X Callisto®	2	31
Formulation + dsRNA T43701 16nmol fb 0.05X Callisto®	49	13

Example 7. A method to control weeds in a field.

[0072] A method to control weeds in a field comprises the use of one or more chloroplast protein import system trigger polynucleotides that can modulate the expression of an endogenous weed gene in one or more target weed plant species. A weed control composition comprising multiple herbicides and multiple polynucleotides can be used in a field environment to control *A. palmeri* plant growth. An analysis of chloroplast protein import system gene sequences from 20 plant species provided a collection of 25-mer polynucleotides (SEQ ID NO: 1264-1483) that can be used in compositions to affect the growth or develop or sensitivity to glyphosate herbicide to control multiple weed species in a field. A composition containing 1 or 2 or 3 or 4 or more of the polynucleotides of SEQ ID NO: 1264-1483 or at least one polynucleotide of at least 19 contiguous polynucleotides and at least 85 percent identical to SEQ ID NO: 1264-1483 that would enable broad activity of the composition against the multiple weed species or variant populations that occur in a field environment.

[0073] The method additionally includes creating an agricultural chemical composition that comprises components that include at least one polynucleotide of of at least 19 contiguous polynucleotides and at least 85 percent identical to SEQ ID NO: 1-1263 or SEQ ID NO: 1584-1638 any other effective gene expression modulating polynucleotide essentially identical or essentially complementary to SEQ ID NO:1-1263 or SEQ ID NO: 1584-1640 fragment thereof and a transfer agent that mobilizes the polynucleotide into a plant cell and a glyphosate containing herbicide and optionally a polynucleotide that modulates the expression of an essential gene and optionally a herbicide that has a different mode of action relative to glyphosate. The polynucleotide of the composition includes a dsRNA, ssDNA or dsDNA or a combination thereof. A composition containing a polynucleotide can have a use rate of about 1 to 30 grams or more per acre depending on the size of the polynucleotide and the number of polynucleotides in the composition. The composition may include one or more additional herbicides as needed to provide effective multi-species weed control. For example, a composition comprising an chloroplast protein import system gene trigger polynucleotide, the composition further including a co-herbicide that includes, but not limited to acetochlor, acifluorfen, acifluorfen-sodium, aclonifen, acrolein, alachlor, alloxymdim, allyl alcohol, ametryn, amicarbazone, amidosulfuron, aminopyralid, amitrole, ammonium sulfamate, anilofos, asulam, atraton, atrazine, azimsulfuron, BCPC, beflubutamid, benazolin, benfluralin, benfuresate, bensulfuron, bensulfuron-methyl, bensulide, bentazone, benzfendazole, benzobicyclon, benzofenap, bifenox, bilanafos, bispyribac, bispyribac-sodium, borax, bromacil, bromobutide, bromoxynil, butachlor, butafenacil, butamifos, butralin, butoxydim, butylate, cacodylic acid, calcium chlorate, cafenstrole, carbetamide, carfentrazone, carfentrazone-ethyl, CDEA, CEPC, chlorflurenol, chlorflurenol-methyl, chloridazon, chlorimuron, chlorimuron-ethyl, chloroacetic acid, chlorotoluron, chlorpropham, chloresulfuron, chlorthal, chlorthal-dimethyl, cinidon-ethyl, cinmethylin, cinosulfuron, cisanilide, clethodim, clodinafop, clodinafop-propargyl, clomazone, clomeprop, clopyralid, cloransulam, cloransulam-methyl, CMA, 4-CPB, CPMF, 4-CPP, CPPC, cresol, cumyluron, cyanamide, cyanazine, cycloate, cyclosulfamuron, cycloxydim, cyhalofop, cyhalofop-butyl, 2,4-D, 3,4-DA, daimuron, dalapon, dazomet, 2,4-DB, 3,4-DB, 2,4-DEB, desmedipham, dicamba, dichlobenil, ortho-dichlorobenzene, para-dichlorobenzene, dichlorprop, dichlorprop-P, diclofop, diclofop-methyl, diclosulam, difenzoquat, difenzoquat metilsulfate, diflufenican, diflufenzopyr, dimefuron, dimepiperate, dimethachlor, dimethametryn, dimethenamid, dimethenamid-P, dimethipin, dimethylarsinic acid, dinitramine, dinoterb, diphenamid, diquat, diquat dibromide, dithiopyr, diuron, DNOC, 3,4-DP, DSMA, EBEP, endothal, EPTC, esprocarb, ethalfluralin, ethametsulfuron, ethametsulfuron-methyl, ethofumesate, ethoxyfen, ethoxysulfuron, etobenzanid, fenoxaprop-P, fenoxaprop-P-ethyl, fentrazamide, ferrous sulfate, flamprop-M, flazasulfuron, florasulam, fluazifop, fluazifop-butyl, fluazifop-P, fluazifop-P-butyl, flucarbazone, flucarbazone-sodium, flucetosulfuron, fluchloralin, flufenacet, flufenpyr, flufenpyr-ethyl, flumetsulam, flumiclorac, flumiclorac-pentyl, flumioxazin, fluometuron, fluoroglycofen, fluoroglycofen-ethyl, flupropanate, flupyrsulfuron, flupyrsulfuron-methyl-sodium, flurenol, fluridone, fluorchloridone, fluoroxypyr, flurtamone, fluthiacet, fluthiacet-methyl, fomesafen, foramsulfuron, fosamine, glufosinate, glufosinate-ammonium, halosulfuron, halosulfuron-methyl, haloxyfop, haloxyfop-P, HC-252, hexazinone, imazamethabenz, imazamethabenz-methyl, imazamox, imazapic, imazapyr, imazaquin, imazethapyr, imazosulfuron, indanofan, iodomethane, iodosulfuron, iodosulfuron-methyl-sodium, ioxynil, isoproturon, isouron, isoxaben, isoxachlortole, isoxaflutole, karbutilate, lactofen, lenacil, linuron, MAA, MAMA, MCPA, MCPA-thioethyl, MCPB, mecoprop, mecoprop-P, mefenacet, mefluidide, mesosulfuron, mesosulfuron-methyl, mesotri- one, metam, metamifop, metamitron, metazachlor, methabenzthiazuron, methylarsonic acid, methylidymron, methyl isothiocyanate, metobenzuron, metolachlor, S-metolachlor, metosulam, metoxuron, metribuzin, metsulfuron, metsulfuron-methyl, MK-66, molinate, monolinuron, MSMA, naproanilide, napropamide, naptalam, neburon, nicosulfuron, nonanoic acid, norflurazon, oleic acid (fatty acids), orbencarb, orthosulfamuron, oryzalin, oxadiargyl, oxadiazon, oxasulfuron, oxaziclonofone, oxyfluorfen, paraquat, paraquat dichloride, pebulate, pendimethalin, penoxsulam, pentachlorophenol, pentanochlor, pentoxazone, pethoxamid, petroleum oils, phenmedipham, phenmedipham-ethyl, picloram, picolnafen, pinoxaden, piperophos, potassium arsenite, potassium azide, pretilachlor, primisulfuron, primisulfuron-methyl, prodiamine, proflumazone, profoxydim, prometon, prometryn, propachlor, propanil, propaquizafop, propazine, propham, propisochlor, propoxycarbazine, propoxycarbazine-sodium, propyzamide, prosulfocarb, prosulfuron, pyraclostrobin, pyraflufen, pyraflufen-ethyl, pyrazolynate, pyrazosulfuron, pyrazosulfuron-ethyl, pyrazoxyfen, pyribenzoxim, pyributicarb, pyridafol, pyridate, pyrifthalid, pyriminobac, pyriminobac-methyl, pyrimisulfan, pyriithiobac, pyriithiobac-sodium, quin-

clorac, quinmerac, quinclamine, quizalofop, quizalofop-P, rimsulfuron, sethoxydim, siduron, simazine, simetryn, SMA, sodium arsenite, sodium azide, sodium chlorate, sulcotrione, sulfentrazone, sulfometuron, sulfometuron-methyl, sulfosate, sulfosulfuron, sulfuric acid, tar oils, 2,3,6-TBA, TCA, TCA-sodium, tebuthiuron, tepraloxym, terbacil, terbutolone, terbutylazine, terbutryn, thenylchlor, thiazopyr, thifensulfuron, thifensulfuron-methyl, thiobencarb, tiocarbazon, topramezone, tralkoxydim, tri-allate, triasulfuron, triaziflam, tribenuron, tribenuron-methyl, tricamba, triclopyr, trietazine, trifloxysulfuron, trifloxysulfuron-sodium, trifluralin, triflurosulfuron, triflurosulfuron-methyl, trihydroxytriazine, tritosulfuron, [3-[2-chloro-4-fluoro-5-(-methyl-6-trifluoromethyl-2,4-dioxo-2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetic acid ethyl ester (CAS RN 353292-3-6), 4-[(4,5-dihydro-3-methoxy-4-methyl-5-oxo)-H-2,4-triazol-yl]carbonyl-sulfamoyl]-5-methylthiophene-3-carboxylic acid (BAY636), BAY747 (CAS RN 33504-84-2), topramezone (CAS RN 2063-68-8), 4-hydroxy-3-[[2-[(2-methoxyethoxy)methyl]-6-(trifluoro-methyl)-3-pyridinyl]carbonyl]-bicyclo[3.2.1]oct-3-en-2-one (CAS RN 35200-68-5), and 4-hydroxy-3-[[2-(3-methoxypropyl)-6-(difluoromethyl)-3-pyridinyl]carbon-yl]-bicyclo[3.2.1]oct-3-en-2-one.

[0074] A field of crop plants in need of weed plant control is treated by spray application of the composition. The composition can be provided as a tank mix, a sequential treatment of components (generally the polynucleotide followed by the herbicide), a simultaneous treatment or mixing of one or more of the components of the composition from separate containers. Treatment of the field can occur as often as needed to provide weed control and the components of the composition can be adjusted to target specific weed species or weed families.

Example 8. Herbicidal Compositions comprising pesticidal agents

[0075] A method of controlling weeds and plant pest and pathogens in a field of glyphosate tolerant crop plants is provided, by applying a herbicidal composition having a polynucleotide, an organosilicone surfactant (about 0.1 percent or greater), and a nonpolynucleotide herbicide and a pest control agent. The polynucleotide is essentially identical or essentially complementary to a segment of a gene sequence that is a component of a chloroplast protein import system of one or more of the target weed species. The trigger oligonucleotide is at least 19 nucleotides in length and at least 85 percent identical to a segment of a gene sequence of SEQ ID NO: 1-1263 and 1584-1638 isolated from a weed species. The nonpolynucleotide herbicide is preferably a glyphosate composition and the pest control agent is preferably an insecticide, fungicide, nematocide, bactericide, acaricide, growth regulator, chemosterilant, semiochemical, repellent, attractant, pheromone, feeding stimulant or other biologically active compounds or biological agents, such as, microorganisms.

[0076] For example, the admixture comprises a fungicide compound for use on a glyphosate tolerant crop plant to prevent or control plant disease caused by a plant fungal pathogen. The fungicide compound of the admixture may be a systemic or contact fungicide or mixtures of each. More particularly the fungicide compound includes, but is not limited to members of the chemical groups: strobilurins, triazoles, chloronitriles, carboxamides and mixtures thereof. The composition may additionally have an admixture comprising an insecticidal compound or agent.

[0077] The chloroplast protein import system trigger polynucleotides and WeatherMAX® (WMAX) tank mixes with fungicides, insecticides or both are tested for use in soybean. Soybean rust is a significant problem disease in South America and serious concern in the U.S. Testing is conducted to develop a method for use of mixtures of the WMAX formulation and various commercially available fungicides for weed control and soy rust control. The field plots are planted with Roundup Ready® soybeans. All plots receive a post plant application of the EPSPS trigger +WMAX about 3 weeks after planting. The mixtures of trigger +WMAX or trigger +WMAX + fungicide + insecticides are used to treat the plots at the R1 stage of soybean development (first flowering) of treatment. Data is taken for percent weed control at 7 and 21 days after R1 treatment, soybean safety (percent necrosis, chlorosis, growth rate): 5 days after treatment, disease rating, and soybean yield (bushels/Acre). These mixtures and treatments are designed to provide simultaneous weed and pest control of soybean, such as fungal pest control, for example, soybean rust disease; and insect pest control, for example, aphids, armyworms, loopers, beetles, stinkbugs, and leaf hoppers.

[0078] Agricultural chemicals are provided in containers suitable for safe storage, transportation and distribution, stability of the chemical compositions, mixing with solvents and instructions for use. A container of a mixture of a trigger oligonucleotide + glyphosate + fungicide compound, or a mixture of a trigger oligonucleotide + glyphosate compound and an insecticide compound, or a trigger oligonucleotide + a glyphosate compound and a fungicide compound and an insecticide compound (for example, lambda-cyhalothrin, Warrior®). The container may further provide instructions on the effective use of the mixture. Containers of the present embodiments can be of any material that is suitable for the storage of the chemical mixture. Containers of the present embodiments can be of any material that is suitable for the shipment of the chemical mixture. The material can be of cardboard, plastic, metal, or a composite of these materials. The container can have a volume of 0.5 liter, 1 liter, 2 liter, 3-5 liter, 5-10 liter, 10-20 liter, 20-50 liter or more depending upon the need. A tank mix of a trigger oligonucleotide + glyphosate compound and a fungicide compound is provided, methods of application to the crop to achieve an effective dose of each compound are known to those skilled in the art and can be refined and further developed depending on the crop, weather conditions, and application equipment used.

[0079] Insecticides, fungicides, nematocides, bactericides, acaricides, growth regulators, chemosterilants, semiochemicals, repellents, attractants, pheromones, feeding stimulants or other biologically active compounds can be added to the trigger oligonucleotide to form a multi-component pesticide giving an even broader spectrum of agricultural protection. Examples of such agricultural protectants with which compounds of the present embodiments can be formulated are: insecticides such as abamectin, acephate, azinphos-methyl, bifenthrin, buprofezin, carbofuran, chlorfenapyr, chlorpyrifos, chlorpyrifos-methyl, cyfluthrin, beta-cyfluthrin, cyhalothrin, lambda-cyhalothrin, deltamethrin, diafenthiuron, diazinon, diflubenzuron, dimethoate, esfenvalerate, fenoxycarb, fenpropathrin, fenvalerate, fipronil, flucythrinate, tau-fluvalinate, fonophos, imidacloprid, isofenphos, malathion, metaldehyde, methamidophos, methidathion, methomyl, methoprene, methoxychlor, methyl 7-chloro-2,5-dihydro-2-[[N-(methoxycarbonyl)-N-[4-(trifluoromethoxy)phenyl]amino]carbonyl]indeno[1,2-e][1,3,4]oxadiazine-4a(3H)-carboxylate (DPX-JW062), monocrotophos, oxamyl, parathion, parathion-methyl, permethrin, phorate, phosalone, phosmet, phosphamidon, pirimicarb, profenofos, rotenone, sulprofos, tebufenozide, tefluthrin, terbufos, tetrachlorvinphos, thiodicarb, tralomethrin, trichlorfon and triflumuron; most preferably a glyphosate compound is formulated with a fungicide compound or combinations of fungicides, such as azoxystrobin, benomyl, blastidicin-S, Bordeaux mixture (tribasic copper sulfate), bromuconazole, captan, captan, carbendazim, chloroneb, chlorothalonil, copper oxychloride, copper salts, cymoxanil, cyproconazole, cyprodinil (CGA 219417), diclomezine, dicloran, difenoconazole, dimethomorph, diniconazole, diniconazole-M, dodine, edifenphos, epoxiconazole (BAS 480F), famoxadone, fenarimol, fenbuconazole, fenpiclonil, fenpropidin, fenpropimorph, fluazinam, fluquinconazole, flusilazole, flutolanil, flutriafol, folpet, fosetyl-aluminum, furalaxyl, hexaconazole, ipconazole, iprobenfos, iprodione, isoprothiolane, kasugamycin, kresoxim-methyl, mancozeb, maneb, mepronil, metalaxyl, metconazole, S-methyl 7-benzothiazolecarbothioate (CGA 245704), myclobutanil, neosazolin (ferric methanearsonate), oxadixyl, penconazole, pencycuron, probenazole, prochloraz, propiconazole, pyrifenoxy, pyroquilon, quinoxifen, spiroxamine (KWG4168), sulfur, tebuconazole, tetraconazole, thiabendazole, thiophanate-methyl, thiram, triadimefon, triadimenol, tricyclazole, trifloxystrobin, triticonazole, validamycin and vinclozolin; combinations of fungicides are common for example, cyproconazole and azoxystrobin, difenoconazole, and metalaxyl-M, fludioxonil and metalaxyl-M, mancozeb and metalaxyl-M, copper hydroxide and metalaxyl-M, cyprodinil and fludioxonil, cyproconazole and propiconazole; commercially available fungicide formulations for control of Asian soybean rust disease include, but are not limited to Quadris® (Syngenta Corp), Bravo® (Syngenta Corp), Echo 720® (Sipcam Agro Inc), Headline® 2.09EC (BASF Corp), Tilt® 3.6EC (Syngenta Corp), PropiMax™ 3.6EC (Dow AgroSciences), Bumper® 41.8EC (MakhteshimAgan), Folicur® 3.6F (Bayer CropScience), Laredo® 25EC (Dow AgroSciences), Laredo™ 25EW (Dow AgroSciences), Stratego® 2.08F (Bayer Corp), Domark™ 125SL (Sipcam Agro USA), and Pristine®38%WDG (BASF Corp) these can be combined with glyphosate compositions as described herein to provide enhanced protection from soybean rust disease; nematocides such as aldoxycarb and fenamiphos; bactericides such as streptomycin; acaricides such as amitraz, chinomethionat, chlorobenzilate, cyhexatin, dicofol, dienochlor, etoxazole, fenazaquin, fenbutatin oxide, fenpropathrin, fenpyroximate, hexythiazox, propargite, pyridaben and tebufenpyrad; and biological agents such as *Bacillus thuringiensis*, *Bacillus thuringiensis* delta endotoxin, baculovirus, and entomopathogenic bacteria, virus and fungi.

Claims

1. A composition for topical application to a surface of a plant comprising a polynucleotide and an organosilicone surfactant, wherein the polynucleotide is identical or complementary to at least 21 contiguous nucleotides of a sequence of a gene of the plant that encodes a polypeptide that is a component of a chloroplast protein import system selected from the group consisting of a translocon at the outer envelope membrane of a chloroplast (TOC), a translocon at the inner envelope membrane of a chloroplast (TIC), a stroma processing peptidase (SPP), and a chaperone like protein associated with the chloroplast protein import system, wherein the polynucleotide is selected from the group consisting of SEQ ID NOs: 1264-1583, 1639 and 1640, and upon a topical application of the composition to the surface of the plant, the composition suppresses the expression of the gene in the plant, thereby making the plant more sensitive to glyphosate, relative to a plant not treated with the polynucleotide.
2. The composition of claim 1, further comprising a pesticide, wherein said pesticide is selected from the group consisting of insecticides, fungicides, nematocides, bactericides, acaricides, growth regulators, chemosterilants, semiochemicals, repellents, attractants, pheromones, feeding stimulants, biopesticides and a combination thereof.
3. A method of plant control comprising: topically applying to a surface of a plant a composition comprising a polynucleotide and an organosilicone surfactant, wherein the polynucleotide is identical or complementary to at least 21 contiguous nucleotides of a sequence of a gene of the plant that encodes a polypeptide that is a component of a chloroplast protein import system selected from the group consisting of a translocon at the outer envelope membrane

of a chloroplast (TOC), a translocon at the inner envelope membrane of a chloroplast (TIC), a stroma processing peptidase (SPP), and a chaperone like protein associated with the chloroplast protein import system, wherein the polynucleotide is selected from the group consisting of SEQ ID NOs: 1264-1583, 1639 and 1640, and wherein the composition suppresses the expression of the gene in the plant, thereby making the plant more sensitive to glyphosate, relative to a plant not treated with the polynucleotide.

Patentansprüche

1. Zusammensetzung zur topischen Anwendung auf einer Oberfläche einer Pflanze, die ein Polynukleotid und ein siliciumorganisches Tensid umfasst, wobei das Polynukleotid identisch oder komplementär zu mindestens 21 aufeinanderfolgenden Nukleotiden einer Sequenz eines Gens der Pflanze ist, das für ein Polypeptid kodiert, das ein Bestandteil des Chloroplastenprotein-Importsystems ist und aus der Gruppe bestehend aus einem Translocon der äußeren Hüllmembran eines Chloroplasten (TOC), einem Translocon der inneren Hüllmembran eines Chloroplasten (TIC), einer Stroma-verarbeitenden Peptidase (SPP) und einem Chaperon-ähnlichen Protein, das mit dem Chloroplastenprotein-Importsystem assoziiert ist, ausgewählt wurde, wobei das Polynukleotid aus der Gruppe bestehend aus SEQ ID NOs: 1264-1583, 1639 und 1640 ausgewählt wurde, und die Zusammensetzung nach topischer Anwendung auf die Oberfläche der Pflanze die Expression des Gens in der Pflanze unterdrückt, wodurch die Pflanze empfindlicher gegenüber Glyphosat wird im Vergleich zu einer Pflanze, die nicht mit dem Polynukleotid behandelt wurde.
2. Zusammensetzung gemäß Anspruch 1, das ferner ein Pestizid umfasst, wobei das Pestizid aus der Gruppe bestehend aus Insektiziden, Fungiziden, Nematiziden, Bakteriziden, Akariziden, Wachstumsregulatoren, Chemosterilantien, Semiochemikalien, Repellentien, Lockstoffen, Pheromonen, Fütterungsstimulanzien, Biopestiziden und einer Kombination davon ausgewählt wurde.
3. Verfahren zur Kontrolle von Pflanzen, das Schritte umfasst, bei denen man eine Zusammensetzung, die ein Polynukleotid und siliciumorganisches Tensid umfasst, auf eine Oberfläche einer Pflanze topisch aufbringt, wobei das Polynukleotid aus mindestens 21 aufeinanderfolgenden Nukleotiden einer Sequenz eines Gens der Pflanze besteht, das für ein Polypeptid kodiert, das identisch oder komplementär zu einem Polypeptid ist, das ein Bestandteil des Chloroplastenprotein-Importsystems ist und aus der Gruppe bestehend aus einem Translocon der äußeren Hüllmembran eines Chloroplasten (TOC), einem Translocon der inneren Hüllmembran eines Chloroplasten (TIC), einer Stroma-verarbeitenden Peptidase (SPP) und einem Chaperon-ähnlichen Protein, das mit dem Chloroplastenprotein-Importsystem assoziiert ist, ausgewählt wurde, wobei das Polynukleotid aus der Gruppe bestehend aus SEQ ID NOs: 1264-1583, 1639 und 1640 ausgewählt wurde, und die Zusammensetzung nach topischer Anwendung auf die Oberfläche der Pflanze die Expression des Gens in der Pflanze unterdrückt, wodurch die Pflanze empfindlicher gegenüber Glyphosat wird im Vergleich zu einer Pflanze, die nicht mit dem Polynukleotid behandelt wurde.

Revendications

1. Composition pour application topique sur une surface d'un végétal, comprenant un polynucléotide et un tensioactif de type organo-silicone, dans laquelle le polynucléotide est identique à, ou complémentaire de, au moins 21 nucléotides contigus d'une séquence d'un gène du végétal qui code un polypeptide qui est un composant d'un système d'import de protéines dans les chloroplastes, choisi dans l'ensemble formé par un translocon (TOC) présent au niveau de la membrane externe d'enveloppe d'un chloroplaste, un translocon (TIC) présent au niveau de la membrane interne d'enveloppe d'un chloroplaste, une peptidase (SPP) agissant dans le stroma, et une protéine de type chaperonne associée au système d'import de protéines dans les chloroplastes, étant entendu que le polynucléotide est choisi dans l'ensemble formé par les Séquences N° 1264 à 1583, 1639 et 1640, et qu'à la suite de l'application topique de la composition sur la surface du végétal, la composition supprime l'expression du gène chez le végétal, rendant ainsi le végétal plus sensible au glyphosate, par comparaison avec un végétal qui n'a pas été traité avec le polynucléotide.
2. Composition conforme à la revendication 1, qui comprend en outre un pesticide, lequel pesticide est choisi dans l'ensemble formé par les insecticides, fongicides, nématicides, bactéricides, acaricides, régulateurs de croissance, chimio-stérilisants, agents sémiochimiques, répulsifs, attractifs, phéromones, stimulants alimentaires et biopesticides, ainsi que leurs combinaisons.

3. Procédé de lutte contre des végétaux, comportant l'application topique, sur une surface d'un végétal, d'une composition comprenant un polynucléotide et un tensioactif de type organo-silicone, dans laquelle le polynucléotide est identique à, ou complémentaire de, au moins 21 nucléotides contigus d'une séquence d'un gène du végétal qui code un polypeptide qui est un composant d'un système d'import de protéines dans les chloroplastes, choisi dans l'ensemble formé par un translocon (TOC) présent au niveau de la membrane externe d'enveloppe d'un chloroplaste, un translocon (TIC) présent au niveau de la membrane interne d'enveloppe d'un chloroplaste, une peptidase (SPP) agissant dans le stroma, et une protéine de type chaperonne associée au système d'import de protéines dans les chloroplastes, étant entendu que le polynucléotide est choisi dans l'ensemble formé par les Séquences N° 1264 à 1583, 1639 et 1640, et qu'à la suite de l'application topique de la composition sur la surface du végétal, la composition supprime l'expression du gène chez le végétal, rendant ainsi le végétal plus sensible au glyphosate, par comparaison avec un végétal qui n'a pas été traité avec le polynucléotide.

A. palmeri – Injury rating 14-DAT

OEP80 triggers polynucleotides were applied at 8 nmol/plant; fb 2x WMAX 1 DAT

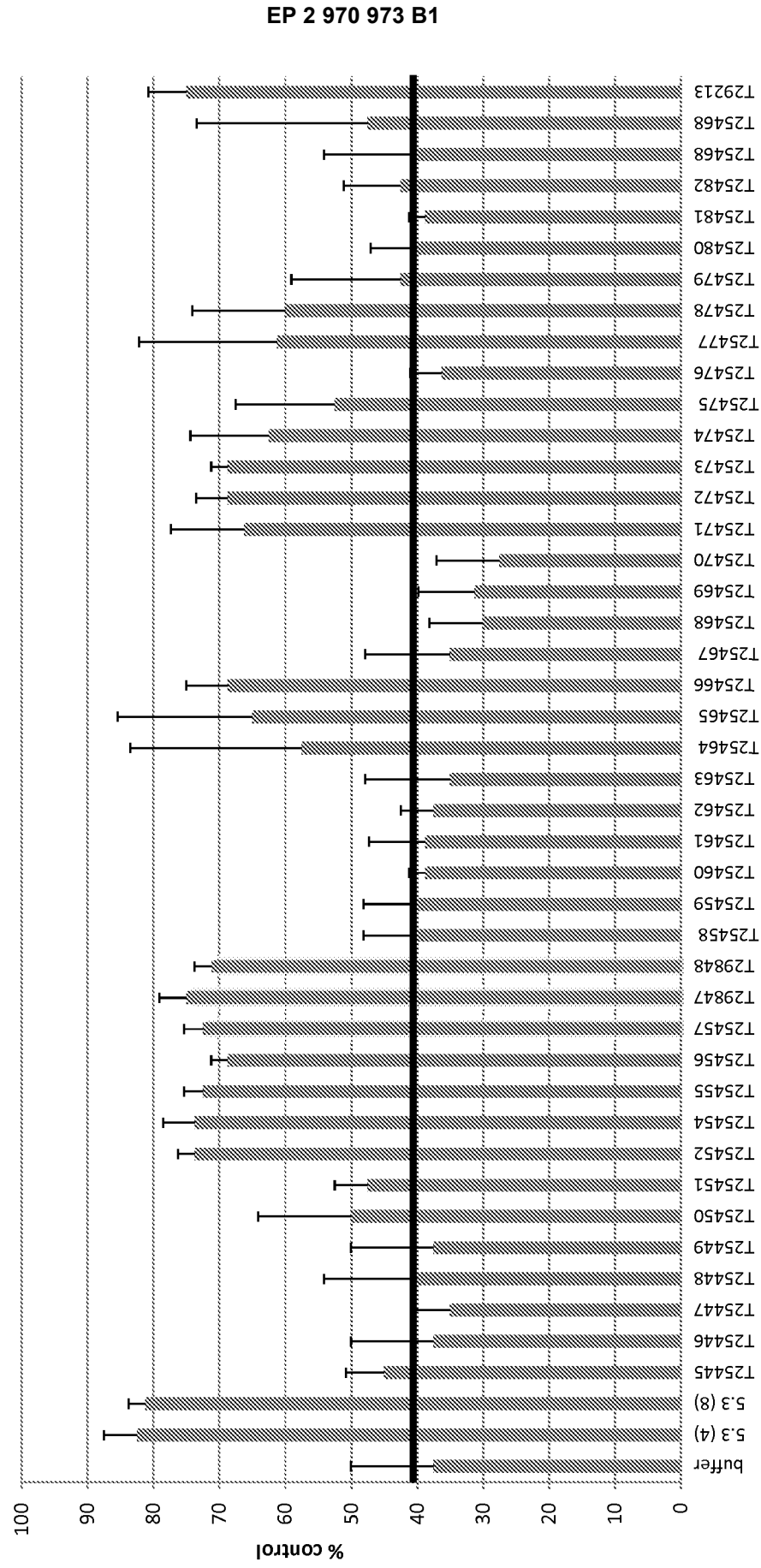


Figure 1

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